

STIC-Biotech/ChemLib

153748

mej

From: Hutzell, Paula
Sent: Wednesday, May 18, 2005 7:07 AM
To: Graser, Jennifer; STIC-Biotech/ChemLib
Subject: RE: rush search

RECEIVED
MAY 18 2005
(STIC)

approved

-----Original Message-----

From: Graser, Jennifer
Sent: Tuesday, May 17, 2005 4:48 PM
To: Hutzell, Paula
Subject: rush search
Importance: High

Hi Paula,
Could you please authorize this ~~rush~~ search for an amendment which is due?
Thanks, Jennifer

STIC:
Please search SEQ ID NO: 1 and 2 for Serial No. 10/650,123 in pending and commercial databases.

Thanks,
Jennifer Graser
REM 3B09 (mailbox 3C18)
Art Unit 1645
272-0858

Interference
Search in
Ex Office

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 13:06:08 ; Search time 7006 Seconds
(without alignments)
3631.029 Million cell updates/sec

Title: US-10-650-123-1
Perfect score: 525
Sequence: 1 atgaaaagcacttgcac.....gcgtgcgcgtcaaatctga 525

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.on.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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3	525	100.0	525 1	AF175683	Neisseria meningitidis
4	525	100.0	525 6	C0786532	Sequence
5	525	100.0	525 6	C0814512	Sequence
6	525	100.0	830 1	NM052066	Neisseria meningitidis
7	525	100.0	830 6	AF167414	Sequence
8	521.8	99.4	525 1	AF175678	Neisseria meningitidis
9	521.8	99.4	10057 1	AE002420	Neisseria meningitidis
10	521.8	99.4	349980 6	AX044030	Sequence
11	518.6	98.8	850 1	NM052068	Neisseria meningitidis
12	518.6	98.8	850 6	AF167416	Sequence
13	518.6	98.8	311321 1	NMA322491	Neisseria meningitidis
14	517	98.5	525 1	AF175677	Neisseria meningitidis
15	517	98.5	525 1	AF175679	Neisseria meningitidis
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26	63	12.0	75	6	CQ771466	Sequence
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ALIGNMENTS

RESULT 1	AF175680	Neisseria meningitidis strain M986 surface protein A (nspA) gene, complete cds.	525 bp	DNA	linear	BCT 06-SEP-1999
LOCUS	AF175680					
DEFINITION	AF175680.1	GI:5825535				
ACCESSION	AF175680					
VERSION	AF175680.1	GI:5825535				
KEYWORDS	Neisseria meningitidis					
SOURCE	Neisseria meningitidis					
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.					
REFERENCE	1 (bases 1 to 525)					
AUTHORS	Moe,G.R., Tan,S. and Granoff,D.M.					
TITLE	Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains					
JOURNAL	Infect. Immun. (1999) In press					
REFERENCE	2 (bases 1 to 525)					
AUTHORS	Moe,G.R., Tan,S. and Granoff,D.M.					
TITLE	Direct Submission					
JOURNAL	Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA					
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ORIGIN						

JOURNAL Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

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ORIGIN

Query Match 100.0%; Score 525; DB 1; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4

CQ786532
LOCUS CQ786532
DEFINITION Sequence 1 from Patent WO2004019976.
ACCESSION CQ786532
VERSION CQ786532.1 GI:45721576
KEYWORDS Neisseria meningitidis
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
REFERENCE 1
AUTHORS Biemans, R., Bos, M., Denoel, P., Feron, C., Goraj, K., Poolman, J., Tommassen, J. and Weynants, V.
TITLE Refolding method
JOURNAL Patent: WO 2004020452-A 8 11-MAR-2004

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

REFERENCE

AUTHORS Martin, D. and Rioux, S.
TITLE Pharmaceutical liposomal compositions containing n. Meningitidis derived polypeptides or polynucleotides
JOURNAL Patent: WO 2004019976-A 1 11-MAR-2004;
SHIRE BIOCHEM, INC. (CA)
FEATURES Location/Qualifiers
source 1. .525
/organism="Neisseria meningitidis"
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/strain="608B"
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Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 481 GTCCGTTCCGCGAAGTGTCCGTCGGCTGCGGTCGCTCAAAATCTGA 525

RESULT 5

CQ814512
LOCUS CQ814512
DEFINITION Sequence 8 from Patent WO2004020452.
ACCESSION CQ814512
VERSION CQ814512.1 GI:47603711
KEYWORDS Neisseria meningitidis
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
REFERENCE 1
AUTHORS Biemans, R., Bos, M., Denoel, P., Feron, C., Goraj, K., Poolman, J., Tommassen, J. and Weynants, V.
TITLE Refolding method
JOURNAL Patent: WO 2004020452-A 8 11-MAR-2004

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FEATURES             GlaxoSmithKline Biologicals S.A. (BE) ; Utrecht University (NL)
source               Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.5e-96;
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RESULT 6
NMU52066
LOCUS               830 bp DNA linear BCT 03-SBP-1999
DEFINITION          Neisseria meningitidis outer membrane protein gene, complete cds.
ACCESSION            U52066
VERSION              U52066.1 GI:1518521
KEYWORDS
SOURCE               Neisseria meningitidis
ORGANISM             Neisseria meningitidis
                     Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                     Neisseriaceae; Neisseria.
REFERENCE
AUTHORS             Martin,D., Cadieux,N., Hamel,J. and Brodeur,B.R.
-TITLE              Highly conserved Neisseria meningitidis surface protein confers
                     protection against experimental infection
JOURNAL              J. Exp. Med. 185 (7), 1173-1183 (1997)
MEDLINE              97258610
PUBMED              9104804
REFERENCE
AUTHORS             Planté,M., Cadieux,N., Rioux,C.R., Hamel,J., Brodeur,B.R. and
                     Martin,D.
-TITLE              Antigenic and molecular conservation of the gonococcal NspA protein
JOURNAL              Infect. Immun. 67 (6), 2855-2861 (1999)
MEDLINE              99270944

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10338491
REFERENCE            3 (bases 1 to 830)
AUTHORS             Cadieux,N., Plante,M., Rioux,C.R., Hamel,J., Brodeur,B.R. and
                     Martin,D.
TITLE               Bactericidal and cross-protective activities of a monoclonal
                     antibody directed against Neisseria meningitidis NspA outer
                     membrane protein
JOURNAL              Infect. Immun. 67 (9), 4955-4959 (1999)
MEDLINE              99386904
PUBMED              10456958
REFERENCE            4 (bases 1 to 830)
AUTHORS             Martin,D.
TITLE               Direct Submission
JOURNAL              Submitted (22-MAR-1996) Denis Martin, Department of Microbiology,
                     University Laval, Unite de Vaccinologie, Laboratoire et Service
                     d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705
                     boul Laurier, Ste-Foy, Quebec G1V 4G2, Canada
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Query Match          100.0%; Score 525; DB 1; Length 830;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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VERSION	AR167414.1	GI:17903193	
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SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 830)		
AUTHORS	Brodeur, B.R., Martin, D., Hamel, J. and Rioux, C.		
TITLE	Proteinase K resistant surface protein of neisseria meningitidis		
JOURNAL	Patent: US 6287574-A 11-SEP-2001;		
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	Best Local Similarity 100.0%; Pred. No. 1.5e-96;		
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Db	323	TTCCGCGTGCATTAACGCGCTACAAAACCTATAAGCCCATCCACCGATTTCAAACTT	382
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Qy	301	CTCGGCGCGGCTTTGAGCCTCAACCGGCGCTCCGTTCGACTTGGGCGGCGAGCAGCTTC	360
Db	443	CTCGGCGCGGCTTTGAGCCTCAACCGGCGCTCCGTTCGACTTGGGCGGCGAGCAGCTTC	502
Qy	361	AGCCAAACCTTCATCGGCGTTCGGGCTATTTGACGGGCGTAAAGTATCGGTTACCCCGAAT	420
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Db	623	GTCCGTTCCCGCGAAGTGTCCGTGCGCGTGCAGTCAAAATTTCTGA	667

RESULT 8					
AF175678					
LOCUS	AF175678	525 bp	DNA	linear	BCT 06-SEP-1999
DEFINITION	Neisseria meningitidis strain CU385 surface protein A (nspA) gene, complete cds.				

ACCESSION	AF175678
VERSION	AF175678.1 GI:5825530
KEYWORDS	.
SOURCE	Neisseria meningitidis
ORGANISM	Neisseria meningitidis Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE	Moe,G.R., Tan,S. and Granoff,D.M. Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains Infect. Immun. (1999) In press
AUTHORS	2 (bases 1 to 525)
TITLE	Moe,G.R., Tan,S. and Granoff,D.M. Direct Submission
JOURNAL	Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
FEATURES	Location/Qualifiers 1..525 /organism="Neisseria meningitidis" /mol_type="genomic DNA" /strain="CU385" /db_xref="taxon:487" 1..525 /gene="nspA" 1..525 /gene="nsrP" 1..525 /codon_start=1 /transl_table=11 /product="surface protein A" /protein_id="AAD53281.1" /db_xref="GI:5825531" /translations="MKALATLALPAALAEGSGFVQDAAHAKSSLSGSAKGFSPRSAGVRINDLPADVTRYKNYKAPSTDFLYSIGASAIYDFDTOSPVKPYGLARLSLRNASVDLGSSFSFQTSIGLVLTGSVAVTNPVLDAGRYNYIKGVNTVKTVRSGEUSAGVRVKPF"
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Query Match	99.4%; Score 521.8; DB 1; Length 525;
Best Local Similarity	99.6%; Pred. No. 6.9e-96;
. Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
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Qy	421 GTCGATTGTGATGCGGCTACCGCTACAACCTATACATCGGCAAGTCAACACTGTCAAAAC 480
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Qy	181	TTGCGCGTGCATTACAGCGGCTACAAAACCTATAAAGCCCCCATCCACCGATTTCAACATT	240
Db	9762	TTGCGCGTGCATTACAGCGGCTACAAAACCTATAAAGCCCCCATCCACCGATTTCAACATT	9703
Qy	241	TACAGCATCGGCGCTCCGCGCATTTACGACTTCGCACACCCAAATCGCCCGTCAAAACCGTAT	300
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Qy	481	GTCCGTTCCGGCGAACTGTCGCTCGCGCTCGCGCTCAAAATTTCTGA	525
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<p>RESULT 10 AX044030/c</p> <p>LOCUS 349980 bp DNA linear PAT 24-NOV-2000</p> <p>DEFINITION Sequence 109 from Patent WO0066791.</p> <p>ACCESSION AX044030</p> <p>VERSION AX044030.1 GI:11342914</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p> <p>Neisseria meningitidis</p> <p>Neisseria meningitidis</p> <p>Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;</p> <p>Neisseriaceae; Neisseria.</p>			
REFERENCE	1	Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C., Masiagnoli, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M., Scarlato, V., Rappuoli, R., Frazer, C. M. and Grandi, G.	
TITLE		Neisseria genomic sequences and methods of their use	
JOURNAL		Patent: WO 0066791-A 109 09-NOV-2000;	
FEATURES		CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)	
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 Db 90666 GGTTCCTGCAAGGCTTACGCGCGCATCTCCGAGGCTACCGATCAAGACCTCCGC 90607
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RESULT 11
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 ACCESSION U52068
 VERSION U52068.1 GI:1808966
 SOURCE Neisseria meningitidis
 ORGANISM Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 1 (bases 1 to 850)
 Martin, D.
 Cadieux, N., Plante, M., Rioux, C.R., Hamel, J., Brodeur, B.R. and
 Bactericidal and cross-protective activities of a monoclonal
 antibody directed against Neisseria meningitidis NspA outer
 membrane protein
 Infect. Immun. 67 (9), 4955-4959 (1999)
 JOURNAL
 MEDLINE 99386904
 PUBMED 10456958
 REFERENCE 2 (bases 1 to 850)
 Martin, D.
 Direct Submission
 Submitted (22-MAR-1996) Denis Martin, Department of Microbiology,
 University Laval, Unite de Vaccinologie, Laboratoire et Service
 d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705
 boul Laurier, Ste-Foy, Quebec G1V 4G2, Canada
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 Best Local Similarity 99.2%; Pred. No. 3e-95;
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 Db 328 GGTTCCTGCAAGGCTTACGCGCGCATCTCCGAGGCTACCGATCAAGACCTCCGC 387
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 QY 421 GTCGATTTGATGCGCGCTACCGCTACAACTACATCGGCAAAAGTCAACTGTCAAAAC 480
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 QY 481 GTCGCTTCGCGGAACTGTCGCTGCGCGTCAAAATTCGA 525
 Db 688 GTCGCTTCGCGGAACTGTCGCTGCGCGTCAAAATTCGA 732
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 LOCUS ARI67416 850 bp DNA linear PAT 17-DEC-2001
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 VERSION ARI67416.1 GI:17903195
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 1 (bases 1 to 850)
 Brodeur, B.R., Martin, D., Hamel, J. and Rioux, C.
 Proteinase K resistant surface protein of neisseria meningitidis
 Patent: US 6287574-A 5 11-SEP-2001;
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 Best Local Similarity 99.2%; Pred. No. 3e-95;
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Db	268	GGCGCATCCGGCTTTAGCTCCAGCCGATCGCGACACGCAAAAGCCCTCAAGCTCTTTA	327
Qy	121	GTTTCTGCAAAAGGTTTCAGCCCGCGCATCTTCGCGAGGTTACCGCATCAAGACCTCCGC	180
Db	328	GTTTCTGCAAAAGGTTTCAGCCCGCGCATCTTCGCGAGGTTACCGCATCAAGACCTCCGC	387
Qy	181	TTCCGCGTCGATTAACACGCGCTACAAAACCTATTAAGCCGCCCATCCACGATTTCAAACTT	240
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Qy	421	GTCGATTTGATGCGCGCTACCGCTCAACATACATCGGCAAGTCAACACTGTCAAAAC	480
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LOCUS	Neisseria meningitidis serogroup A strain Z491 complete genome;		
DEFINITION	segment 3/7.		
ACCESSION	AL162754	AL157959	
VERSION	AL162754.2	GI:7379424	
KEYWORDS			
SOURCE	Neisseria meningitidis Z491		
ORGANISM	Neisseria meningitidis Z491		
REFERENCE	1 (bases 1 to 311321)		
AUTHORS	Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C., Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T., Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N., Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K., Quail,M.A., Rajandram,M.A., Rutherford,K.M., Simmonds,M., Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G.		
TITLE	Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z491		
JOURNAL	Nature	404 (6777),	502-506 (2000)
MEDLINE	20222556		
PubMed	10761919		
REFERENCE	2 (bases 1 to 311321)		
AUTHORS	Parkhill,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-MAR-2000)		
COMMENT	Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk		
NOTES	Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.		
URL	(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).		
LOCATION/Qualifiers	1. .311321		
ORGANISM=Neisseria meningitidis Z491"			
FEATURES	source		

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wrbA, Escherichia coli Ttp repressor binding protein (197
aa), fasta scores; E(): 0.064, 29.3% identity in 82 aa
overlap. Also similar to part of TR:O85450 (EMBL:AF067083)
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(124 aa), fasta scores; E(): 6.6e-14, 56.6% identity in 83
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of succinoglycan biosynthesis (not a transcriptional
regulator) (234 aa), fasta scores; E(): 3.1e-15, 32.7%
identity in 205 aa overlap. Also similar to many
bacterial hypothetical proteins e.g. SW:YBAX_HAEIN
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fasta scores; E(): 5.1e-32, 58.0% identity in 138 aa
overlap. Shows very weak similarity to eukaryotic
6-pyruvoyl-tetrahydropterin synthases e.g. SW:PFPS_RAT
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Query Match 98.8%; Score 518.6; DB 1; Length 311321;

Best Local Similarity 99.2%; Pred. No. 2.1e-95;

Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 121 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 180

Db 149737 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 149678

QY 181 TTCGCGCTCGATTACACGGCTTACAAAACATAAAGCCCAATCCACGATTTCAAACTT 240

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QY 301 CTCGCGCGCGCTTGAGGCTCAACCGCGCTCCGTCGACTTGGGGGCGGACGACGCTTC 360

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QY 361 AGCCAAACCTCCATCGGCTCGCGCTATTTAGCGGGGTAAGCTATCCGTTACCCGGAAT 420

Db 149497 AGCCAAACCTCCATCGGCTCGCGCTATTTAGCGGGGTAAGCTATCCGTTACCCGGAAT 149438

QY 421 GTCGATTTGGATGCGCGGTACCGCTACAACTACATCGCAAAAGTCAACACTGTCAAAAAC 480

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RESULT 14

AF175677

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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Neisseria meningitidis strain BZ232 surface protein A (nspA) gene,
complete cds.

AF175677 GI:5825528

Neisseria meningitidis

Neisseria meningitidis

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; Neisseria.

REFERENCE	1 (bases 1 to 525)
AUTHORS	Moe,G.R., Tan,S. and Granoff,D.M.
TITLE	Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains
JOURNAL	Infect. Immun. (1999) In press
REFERENCE	2 (bases 1 to 525)
AUTHORS	Moe,G.R., Tan,S. and Granoff,D.M.
TITLE	Direct Submission
JOURNAL	Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
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Query Match	98.5%; Score 517; DB 1; Length 525;
Best Local Similarity	99.0%; Pred. No. 6.5e-95;
Matches 520; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
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Qy	61 GGCGCATCCGGCTTTTAGCTCAAAGCCGATGCCGCACACGCAAAAAGCCTCAAGCTCTTTTA 120
Db	61 GGCGCATCCGGCTTTTAGCTCAAAGCCGATGCCGCACACGCAAAAAGCCTCAAGCTCTTTTA 120
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Qy	301 CTGGCGCGCGCTTGAGCCTCAACCGCGCTCTCGTTCGACTTGGCGGCGCAGCACGCTTC 360
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Qy	361 AGCCAAACCTCCATCGCCTCGCGTATTGACGGGCGTAAAGCTATGCCGTACCCCGAAT 420
Db	361 AGCCAAACCTCCACCGGCTCGCGTATTGACGGGCGTAAAGCTATGCCGTACCCCGAAT 420
Qy	421 GTCGATTGGATTGCGCGCTACCGGTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
Db	421 GTCGATTGGATGCGCGCTACCGGTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
Qy	481 GTCCGTTCCGCGGAACGTCCGTCGGCGTGGCGTCAAAATCTGA 525
Db	481 GTCCGTTCCGCGGAACGTCCGTCGGCGTGGCGTCAAAATCTGA 525
RESULT	15

RESULT 15

AF175679	AF175679	525 bp	DNA	linear	BCT 06-SEP-1999
LOCUS	Neisseria meningitidis strain M136 surface protein A (nspA) gene, complete cds.				
ACCESSION	AF175679				
VERSION	AF175679.1	GI:5825533			
KEYWORDS	Neisseria meningitidis				
SOURCE	Neisseria meningitidis				
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.				
REFERENCE	1 (bases 1 to 525)				
AUTHORS	Moe,G.R., Tan,S. and Granoff,D.M.				
TITLE	Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains				
JOURNAL	Infect. Immun. (1999) In press				
AUTHORS	2 (bases 1 to 525)				
TITLE	Moe,G.R., Tan,S. and Granoff,D.M.				
JOURNAL	Direct Submission				
FEATURES	Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA				
source	Location/Qualifiers				
	1..525				
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	/strain="M136"				
	/db_xref="taxon:487"				
gene	1..525				
	/gene="nspA"				
CDS	1..525				
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	/codon_start=1				
	/transl_table=11				
	/product="surface protein A"				
	/protein_id="AAD53282.1"				
	/db_xref="GI:5825534"				
	/translation="MKKALATLIALIPAALAEAGSGFYVQADAHAKASSIGSAKGFSPISAGRYINDLRFAYDTRYKNYKAPDFFKLYIGASAIYDFDQSPVKPYLIGARLLSNRASVDLGGSDFSQTSGLGLVTGVSVAVTPNVDLDDAGYRYNYIKGVTVTKNVRSELGSAGRVRFK"				
ORIGIN					
Query Match	98.5%;	Score 517;	DB 1;	Length 525;	
Best Local Similarity	99.0%;	Pred. No. 6.5e-95;			
Matches 520;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;	
Qy	1	ATGAAAAGACACTTGCACACTGATTCGCTCGCTCTCCGCGCGCGCACCTGGCGGAA	60		
Db	1	ATGAAAAGACACTTGCACACTGATTCGCTCGCTCTCCGCGCGCGCACCTGGCGGAA	60		
Qy	61	GGCGCATCCGGCTTTTACGTCCAAAGCCGATGCCGCACACGCAACCAAGCTCTTTA	120		
Db	61	GGCGCATCCGGCTTTTACGTCCAAAGCCGATGCCGCACACGCAACCAAGCTCTTTA	120		
Qy	121	GGTTCCTGCCAAGGCTTCAGCCCGCGCATCTCCGCAAGGCTACCGCATCAACGACCTCCGC	180		
Db	121	GGTTCCTGCCAAGGCTTCAGCCCGCGCATCTCCGCAAGGCTACCGCATCAACGACCTCCGC	180		
Qy	181	TTCCGCGTCGATTACACGGGCTCAAAAACATAAAGCCCCATCCACCGATTTCAAACATT	240		
Db	181	TTCCGCGTCGATTACACGGGCTCAAAAACATAAAGCCCCATCCACCGATTTCAAACATT	240		
Qy	241	TACAGATCGGCGCTCCGCGCATTTACGACTTCGACACCAACCAATCGCCCGTCAACCGTAT	300		
Db	241	TACAGATCGGCGCTCCGCGCATTTACGACTTCGACACCAACCAATCGCCCGTCAACCGTAT	300		
Qy	301	CTCGGCGCGGCTTGAGCCCTCAACCGCGCTCCGTCGACTTGGCGGCGCACGCAAGCTTC	360		
Db	301	CTCGGCGCGGCTTGAGCCCTCAACCGCGCTCCGTCGACTTGGCGGCGCACGCAAGCTTC	360		
Qy	361	AGCCAAACTCCATCCGGCTTCGGCGTATTGACGGGCGTAAAGCTATGCGTTACCCGGAAT	420		
Db	361	AGCCAAACTCCACCGGCTTCGGCGTATTGACGGGCGTAAAGCTATGCGTTACCCGGAAT	420		

Qy	421	GTGATTGGATGCCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCTCAAAAAC	480
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Qy	481	GTCCGTTCCGGCGAACTGTCCGTCGGCGTGC GGTC AAAATTCTGA	525
Db	481	GTCCGTTCCGGCGAACTGTCCGTCGGCGTGC GGTC AAAATTCTGA	525

Search completed: May 19, 2005, 17:22:51
 Job time : 7013 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 12:43:12 ; Search time 1066 Seconds
(without alignments)
2915.445 Million cell updates/sec

Title: US-10-650-123-1

Perfect score: 525

Sequence: 1 atgaaaaagcacttgccac.....gctgctgcgtcaaatctga 525

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525	100.0	525	12 ADL13427	Adl13427 Neisseria
2	525	100.0	525	12 ADL24351	Adl24351 N meningi
3	525	100.0	830	2 AAT39039	Aat39039 Proteinas
4	525	100.0	830	8 ACA64711	Acag4711 N. mening
5	525	100.0	830	10 ADF43315	Adf43315 N. mening
6	521.8	99.4	37668	3 AAA81490_14	Continuation (15 o
7	521.8	99.4	110000	3 AAA81490_06	Continuation (7 of
8	521.8	99.4	349980	3 AAF21608	Aaf21608 Neisseria
9	518.6	98.8	850	2 AAT39041	Aat39041 Proteinas
10	502.6	95.7	710	6 ABS67381	Abse67381 Neisseria
11	502.6	95.7	810	2 AAT39042	Aat39042 Proteinas
12	491.2	93.6	710	2 AAT39040	Aat39040 Proteinas
13	480.2	91.5	525	10 ABZ38961	Abz38961 N. gonorr
14	464.8	88.5	468	12 ADL13425	Adl13425 Neisseria
15	368	70.1	486	10 ABZ38960	Abz38960 N. gonorr
16	63	12.0	75	12 ADJ83984	Adj83984 Neisseria
17	51.4	9.8	985	6 ABQ44816	Abq44816 Oligonuc
18	51.4	9.8	985	6 ABQ44817	Abq44817 Oligonuc
19	49.8	9.5	1919	12 ADM94375	Adm94375 Wheat ABC
20	49.2	9.4	86941	12 ADI39160	Adi39160 Streptomy

21	49	9.3	13631	4	ABL20354	Abl20354 Drosophil
22	48.6	9.3	1682	12	ADJ39303	Adj39303 Plant CDN
23	47	9.0	1842	8	ADA71243	Ada71243 Rice gene
24	46.8	8.9	72	11	ADM40964	Adm40964 Neisseria
25	46.4	8.8	1329	8	ADA69820	Ada69820 Rice gene
26	45.6	8.7	1005	2	AZ330006	Aaz33006 Optimised
27	45.6	8.7	1076	2	AZ330007	Aaz33007 Optimised
28	45.6	8.7	2607	4	ABL16369	Abli16369 Drosophil
29	45.6	8.7	110000	4	RAI99682_37	Continuation (38 o
30	45.6	8.7	110000	4	RAI99683_37	Continuation (38 o
31	45.2	8.6	72	11	ADM40962	Adm40962 Neisseria
32	45	8.6	45	12	ADL24367	Adl24367 N meningi
33	45	8.6	609	9	ACL14692	Ac114692 DNA clone
34	45	8.6	3324	8	ACA38418	Aca38418 Prokaryot
35	45	8.6	9903	8	ACA40315	Aca40315 Prokaryot
36	45	8.6	110000	4	RAI99682_04	Continuation (5 of
37	45	8.6	110000	4	RAI99683_04	Continuation (5 of
38	44.8	8.5	1296	6	ABQ67797	Abq67797 Listeria
39	44.8	8.5	1311	6	ABQ67800	Abq67800 Listeria
40	44.8	8.5	1497	8	ACA40556	Aca40556 Prokaryot
41	44.8	8.5	2905	6	ABQ70634	Abq70634 Listeria
42	44.8	8.5	110000	4	RAI99682_20	Continuation (21 o
43	44.8	8.5	110000	6	ABQ69245_19	Continuation (20 o
44	44.8	8.5	149158	12	ADP74211	Adp74211 Equine he
45	44.8	8.5	149261	12	ADP74212	Adp74212 Equine he

ALIGNMENTS

RESULT 1
ADL13427
ID ADL13427 standard; DNA; 525 BP.
XX
AC ADL13427;
XX
DT 03-JUN-2004 (first entry)
XX
DE Neisseria meningitidis H44/76 Nspa gene.
XX
KW Neisserial surface protein A; Nspa; refolding; recombinant production;
KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;
KW invasive bacterial disease; bacteraemia; meningitis;
KW Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;
KW antibacterial; gene therapy; gene; ds.
XX
OS Neisseria meningitidis; H44/76.
XX

Key Location/Qualifiers
CDS 1..525
FT /*tag= b
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FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..522
FT /*tag= c
FT /product= "Mature Nspa"
XX
XX WO2004020452-A2.
XX
XX 11-MAR-2004.
XX
XX 28-AUG-2003; 2003WO-EP010085.
XX
XX 30-AUG-2002; 2002GB-00020197.
XX
XX (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
XX (UYUT-) RIJKSUNIV UTRECHT.
XX
XX Bienenans R, Bos M, Denoel P, Feron C, Goraj K, Poolman J;
XX Tommassen J, Weynants V;
XX WPI; 2004-239150/22.

DR P-PSDB; ADL13428.

XX New refolded NspA protein, useful for preparing a composition for

PT diagnosing, treating or preventing infection caused by *Neisseria*

PT meningitidis or *Neisseria gonorrhoeae*.

XX

PS Disclosure; Fig 3; 62pp; English.

XX

CC The invention relates to an isolated refolded *Neisseria* surface protein

CC A (NspA) from *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The

CC invention also relates to the method of refolding an NspA protein; an

CC alkaline refolding buffer comprising ethanolamine and SB-12 (3-

CC dimethyladecylammonio)propanesulphonate) for refolding an NspA protein; a

CC pharmaceutical composition comprising the refolded NspA protein, a

CC carrier and optionally one or more other *Neisseria* antigens; a method of

CC preventing or treating a *Neisseria* infection; an antibody immunospecific

CC for the NspA protein; and diagnosing a *Neisseria* infection. NspA has

CC characteristics which indicate that it is a potential vaccine candidate

CC for the development of subunit vaccines for the treatment of infections

CC caused by *Neisseria meningitidis* (meningococcus), which causes invasive

CC bacterial diseases such as bacteraemia and meningitis, or *Neisseria*

CC gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced

CC NspA could therefore be used to produce vaccine compositions and it could

CC also be used in the development of new antimicrobial agents, diagnostic

CC tests and in drug screening. However, recombinantly produced proteins are

CC frequently unable to adopt their biologically active conformations, and

CC yields may be very low due to mis-folding and aggregation of the protein.

CC The method of the invention provides an improved method for refolding the

CC NspA protein, and it is possible to increase the recovery of active

CC protein form partly purified inclusion bodies in amounts up to 100%

CC without the need for further purification. The refolded NspA protein is

CC useful for preparing a composition for diagnosing, treating or preventing

CC infection caused by *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The

CC present sequence represents the NspA gene from *Neisseria meningitidis*

CC H44/76.

XX

SQ Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 12; Length 525;

Best Local Similarity 100.0%; Pred. No. 4.7e-125;

Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGGCACAATGATGCTCCGCGCGCGCTCAAGCTCTTTA 120

DB 1 ATGAAAAAGCACTTGGCACAATGATGCTCCGCGCGCGCTCAAGCTCTTTA 120

QY 61 GGCGCATCGGCTTTTACGTCCAAAGCGATGCGGCACACGCAAAAGCTTCAAGCTCTTTA 120

DB 61 GGCGCATCGGCTTTTACGTCCAAAGCGATGCGGCACACGCAAAAGCTTCAAGCTCTTTA 120

QY 121 GGTCTCTGCCAAGGCTTCAGCGCGCGCATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180

DB 121 GGTCTCTGCCAAGGCTTCAGCGCGCGCATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180

QY 181 TTGCGCGTGAATACACGGCTTACAAAACTATAAAGCCCATTCACACGATTTCAAACTT 240

DB 181 TTGCGCGTGAATACACGGCTTACAAAACTATAAAGCCCATTCACACGATTTCAAACTT 240

QY 241 TACAGCATCGGCGCTTCGCGCATTTACGACTTCGACACCAATCGCGCGTCAACCGTAT 300

DB 241 TACAGCATCGGCGCTTCGCGCATTTACGACTTCGACACCAATCGCGCGTCAACCGTAT 300

QY 301 CTGCGCGCGCTTGAAGCTTCAACCGCGCTTCGTCGACTTGGCGGCGACGACGCTTC 360

DB 301 CTGCGCGCGCTTGAAGCTTCAACCGCGCTTCGTCGACTTGGCGGCGACGACGCTTC 360

QY 361 AGCCAACTCTCATTCGCGCTTGAAGCTTGAAGCGGCTGAAGCTATGCGCGTTACCGCAAT 420

DB 361 AGCCAACTCTCATTCGCGCTTGAAGCTTGAAGCGGCTGAAGCTATGCGCGTTACCGCAAT 420

QY 421 GTCGATTTGATGCGCGGCTACCGCTACAACTACATCGCAAAAGTCAACACTGTCAAAAC 480

DB 421 GTCGATTTGATGCGCGGCTACCGCTACAACTACATCGCAAAAGTCAACACTGTCAAAAC 480

QY 481 GTCCGCTTCGCGCAACTGTCCGTCGCGCTCGCGTCAAAATTTCTGA 525

DB 481 GTCCGCTTCGCGCAACTGTCCGTCGCGCTCGCGTCAAAATTTCTGA 525

RESULT 2

ADL24351

ID ADL24351 standard; DNA; 525 BP.

XX

AC ADL24351;

XX

DT 03-JUN-2004 (first entry)

XX

DE N meningitidis strain 608B NspA coding sequence.

XX

XX ds; gene; NspA; vaccine; antibacterial; meningitis.

XX

OS *Neisseria meningitidis*.

XX

EH Key Location/Qualifiers

CDS 1..525

FT /*tag= a

FT /product= "NspA"

XX

PN WO2004019976-A2.

XX

PD 11-MAR-2004.

XX

PF 29-AUG-2003; 2003WO-CA001452.

XX

PR 30-AUG-2002; 2002US-0406980P.

XX

PA (SHIR-) SHIRE BIOCHEM INC.

XX

PI Martin D, Rioux S;

XX

DR WPI; 2004-239123/22.

DR P-PSDB; ADL24352.

XX

PT Composition comprising liposome associated with isolated polypeptide or

PT polynucleotide derived from *Neisseria meningitidis* strain 608B, or its

PT fragment or analog, useful for inducing an immune response against N.

PT meningitidis.

XX

PS Claim 9; Fig 1; 79pp; English.

XX

CC The present invention relates to a pharmaceutical composition comprising

CC a liposome associated with an isolated polypeptide derived from *Neisseria*

CC meningitidis strain 608B, where the polypeptide is the NspA protein. The

CC composition is useful for inducing an immune response against N.

CC meningitidis, for preventing and/or treating N. meningitidis infection

CC and for treating and/or preventing *Neisseria* infection chosen from N.

CC meningitidis, N. gonorrhoeae, N. lactamica and N. polysacchara. It is

CC useful for treatment or prophylaxis of meningitis and meningococemia, in

CC a host. The host is a mammal, preferably a human and more preferably an

CC adult human. The present sequence is the *Neisseria meningitidis* strain

CC 608B NspA coding sequence.

XX

SQ Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 12; Length 525;

Best Local Similarity 100.0%; Pred. No. 4.7e-125;

Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGGCACAATGATGCTCCGCGCGCGCTCAAGCTCTTTA 60

DB 1 ATGAAAAAGCACTTGGCACAATGATGCTCCGCGCGCGCTCAAGCTCTTTA 60

QY 61 GGCGCATCGGCTTTTACGTCCAAAGCGATGCGGCACACGCAAAAGCTTCAAGCTCTTTA 120

DB 61 GGCGCATCGGCTTTTACGTCCAAAGCGATGCGGCACACGCAAAAGCTTCAAGCTCTTTA 120

QY 121 GGTCTCTGCCAAGGCTTCAGCGCGCGCATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180

DB 121 GGTCTCTGCCAAGGCTTCAGCGCGCGCATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180

QY 181 TTGCGCGTGAATACACGGCTTACAAAACTATAAAGCCCATTCACACGATTTCAAACTT 240

DB 181 TTGCGCGTGAATACACGGCTTACAAAACTATAAAGCCCATTCACACGATTTCAAACTT 240

QY 241 TACAGCATCGGCGCTTCGCGCATTTACGACTTCGACACCAATCGCGCGTCAACCGTAT 300

DB 241 TACAGCATCGGCGCTTCGCGCATTTACGACTTCGACACCAATCGCGCGTCAACCGTAT 300

QY 301 CTGCGCGCGCTTGAAGCTTCAACCGCGCTTCGTCGACTTGGCGGCGACGACGCTTC 360

DB 301 CTGCGCGCGCTTGAAGCTTCAACCGCGCTTCGTCGACTTGGCGGCGACGACGCTTC 360

QY 361 AGCCAACTCTCATTCGCGCTTGAAGCTTGAAGCGGCTGAAGCTATGCGCGTTACCGCAAT 420

DB 361 AGCCAACTCTCATTCGCGCTTGAAGCTTGAAGCGGCTGAAGCTATGCGCGTTACCGCAAT 420

QY 421 GTCGATTTGATGCGCGGCTACCGCTACAACTACATCGCAAAAGTCAACACTGTCAAAAC 480

DB 421 GTCGATTTGATGCGCGGCTACCGCTACAACTACATCGCAAAAGTCAACACTGTCAAAAC 480

QY 121 GGTTCGCAAGGCTTCAGCCCGGCTATCTCCGAGGCTACCGCATCAAGACCTCCGC 180
 DB 121 GGTTCGCAAGGCTTCAGCCCGGCTATCTCCGAGGCTACCGCATCAAGACCTCCGC 180
 QY 181 TTCGCGCTCGATTACACGGCTACAAAACTATAAGCCCATCCACCGATTTCAAACTT 240
 DB 181 TTCGCGCTCGATTACACGGCTACAAAACTATAAGCCCATCCACCGATTTCAAACTT 240
 QY 241 TACAGCATCGCGCTCGCCATTTCAGCTTCGACACCCCAATCGCCGTCAAAACCGTAT 300
 DB 241 TACAGCATCGCGCTCGCCATTTCAGCTTCGACACCCCAATCGCCGTCAAAACCGTAT 300
 QY 301 CTCGCGCGCTTCAGCTTCACCGCGCTTCAGCTTCGAGCTGGGGGCGAGCAGCTTC 360
 DB 301 CTCGCGCGCTTCAGCTTCACCGCGCTTCAGCTTCGAGCTGGGGGCGAGCAGCTTC 360
 QY 361 AGCCAAACCTCATCGGCTCGCGCTATTGACGGCGCTAAGCTATGCCGTTACCCCGAAT 420
 DB 361 AGCCAAACCTCATCGGCTCGCGCTATTGACGGCGCTAAGCTATGCCGTTACCCCGAAT 420
 QY 421 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
 DB 421 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
 QY 481 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAAAATTCTGA 525
 DB 481 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAAAATTCTGA 525

RESULT 3

ID AAT39039 standard; DNA; 830 BP.

AC AAT39039;

XX 16-OCT-2003 (revised)
 DT 22-DEC-1996 (first entry)

Proteinase K resistant N. meningitidis 22 kD surface protein.

Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
 antibody; detection; probe; surface protein; ss.

Neisseria meningitidis; strain 608B.

Key	Location/Qualifiers
FT -10_signal	75..80
FT RBS	/*tag= d
FT CDS	131..135
FT sig_peptide	/*tag= e
FT mat_peptide	143..167
FT	/*tag= a
FT	143..199
FT	/*tag= b
FT	200..664
FT	/*tag= c

PN WO9629412-A1.

XX 26-SEP-1996.

XX 15-MAR-1996; 96WO-CA000157.

XX 17-MAR-1995; 95US-00406362.

XX 04-AUG-1995; 95US-0001983P.

XX (IAFB-) IAF BIO VAC INC.

XX Brodeur BR, Martin D, Hamel J, Rioux C;

XX WPI; 1996-443187/44.

XX P-PSDB; AAW04891.

XX

PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against, or
 PT diagnosis of, N. meningitidis infection.

PS Claim 12; Fig 1; 117pp; English.

XX A proteinase K resistant surface protein has been isolated from 4 strains
 CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
 CC antigenic fragments of antibodies can be used in a vaccine for the
 CC prevention of infection by N. meningitidis or by N. gonorrhoeae in
 CC humans. The antibodies may also be used diagnostically to detect N.
 CC meningitidis infection. The antigen may also be used to detect antibodies
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,
 CC or their fragments, can be used as probes for the detection of pathogenic
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 2; Length 830;
 Best Local Similarity 100.0%; Pred. No. 5.3e-125;
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGCACACTGATTCCTCTCCCGCGCGCGCACTGCGGAA 60
 DB 143 ATGAAAAAGCACTTGCACACTGATTCCTCTCCCGCGCGCGCACTGCGGAA 202
 QY 61 GCGCATCCGGCTTTTACGTCCAAAGCGATCCGACACGCAAAAGCTTCAAGCTTTTA 120
 DB 203 GCGCATCCGGCTTTTACGTCCAAAGCGATCCGACACGCAAAAGCTTCAAGCTTTTA 262
 QY 121 GGTTCGCAAGGCTTCAGCCCGGCTATCTCCGAGGCTACCGCATCAAGACCTCCGC 180
 DB 263 GGTTCGCAAGGCTTCAGCCCGGCTATCTCCGAGGCTACCGCATCAAGACCTCCGC 322
 QY 181 TTCGCGCTCGATTACACGGCTACAAAACTATAAGCCCATCCACCGATTTCAAACTT 240
 DB 323 TTCGCGCTCGATTACACGGCTACAAAACTATAAGCCCATCCACCGATTTCAAACTT 382
 QY 241 TACAGCATCGCGCTCGCCATTTCAGCTTCGACACCCCAATCGCCGTCAAAACCGTAT 300
 DB 383 TACAGCATCGCGCTCGCCATTTCAGCTTCGACACCCCAATCGCCGTCAAAACCGTAT 442
 QY 301 CTCGCGCGCTTCAGCTTCACCGCGCTTCAGCTTCGAGCTGGGGGCGAGCAGCTTC 360
 DB 443 CTCGCGCGCTTCAGCTTCACCGCGCTTCAGCTTCGAGCTGGGGGCGAGCAGCTTC 502
 QY 361 AGCCAAACCTCATCGGCTCGCGCTATTGACGGCGCTAAGCTATGCCGTTACCCCGAAT 420
 DB 503 AGCCAAACCTCATCGGCTCGCGCTATTGACGGCGCTAAGCTATGCCGTTACCCCGAAT 562
 QY 421 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
 DB 563 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 622
 QY 481 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAAAATTCTGA 525
 DB 623 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAAAATTCTGA 667

RESULT 4

ID ACA64711 standard; DNA; 830 BP.

AC ACA64711;

DT 18-JUN-2003 (first entry)

DE N. meningitidis lipopolysaccharide gene.

XX Superantigen; ds; gene; SAG; staphylococcal enterotoxin; tumour; cancer;
 KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.

XX OS Neisseria meningitidis.

XX PN US2002177551-A1.

XX PD 28-NOV-2002.

XX PF 30-MAY-2001; 2001US-00870759.

XX PR 31-MAY-2000; 2000US-0208128P.

XX PA (TERM/) TERMAN D S.

XX PI Terman DS;

XX DR WPI; 2003-361759/34.

XX DR P-PSDB; ABU9079.

XX PT A mammalian cell receptor, useful in the treatment of cancer by binding

XX PT to tumor associated lipids where the binding induces energy or apoptosis

XX PT in T cells and antigen presenting cells.

XX PS Disclosure; Page; 167pp; English.

XX CC The invention relates to a mammalian cell receptor, useful in the

XX CC treatment of cancer, which binds to tumor associated lipids and induces

XX CC energy or apoptosis in the T cells and antigen presenting cells (APCs).

XX CC Also included are a mammalian cell useful in the treatment of cancer

XX CC where the receptor which binds tumor associated lipids and induces

XX CC cellular inactivation or death is deleted or functionally deactivated,

XX CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal

XX CC (by allowing tumour associated lipids to contact immunocytes in which

XX CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,

XX CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,

XX CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or

XX CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell

XX CC useful in the treatment of cancer (where an adaptor protein which

XX CC inhibits T cell activation by tumour associated antigens is deleted or

XX CC functionally deactivated), a composition useful in the treatment of

XX CC cancer (comprising a lipid raft conjugated to a superantigen), producing

XX CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by

XX CC allowing tumour associated lipids to contact immunocytes, in which

XX CC receptors for the lipids are inactivated or deleted to produce a

XX CC tumouricidal immunocyte population, and administering the tumouricidal APC

XX CC activated immunocytes to the host), producing (M3) a tumouricidal APC

XX CC population ex vivo in a mammal (by allowing a tumour associated lipid to

XX CC contact APCs, in which receptors for the tumour associated lipids are

XX CC inactivated or deleted to produce a tumouricidally activated population,

XX CC and administering APCs to the host), producing a tumouricidal T cell

XX CC population ex vivo in a mammal (by allowing a tumour associated lipids to

XX CC contact T cells, in which adaptor proteins, which inhibit T cell

XX CC activation by tumour associated antigens, are deleted or functionally

XX CC deactivated to produce a tumouricidal population of T cells, and

XX CC administering the tumouricidally activated T cells to the host, or

XX CC allowing a superantigen-lipid raft to contact T cells ex vivo, and

XX CC administering the tumouricidally activated T cells to the host), treating

XX CC (M5) cancer in a mammal (by administering a lipid binding molecule which

XX CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)

XX CC a tumouricidal T cell population in vivo in a mammal (by allowing a

XX CC tumour associated antigen to contact immunocytes in which adaptor

XX CC proteins which inhibit T cell activation by tumour associated antigens

XX CC are deleted or functionally deactivated) and producing (M7) a

XX CC tumouricidal T cell population ex vivo in a mammal comprising allowing a

XX CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The

XX CC receptors, methods and compositions are useful for treating cancers and

XX CC tumours. Bacterial superantigens are co-administered or administered as

XX CC fusion constructs with anti-tumour proteins or motifs. The present

XX CC sequence encodes an anti-tumour protein which is co-administered with or

XX CC incorporated into a fusion construct with a superantigen. Note: The

XX CC sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format from the US patent

XX CC office website at "seqdata.uspto.gov/sequence.html?docID=20020177551"

XX SQ Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 8; Length 830;

Best Local Similarity 100.0%; Pred. No. 5.3e-125; Indels 0; Gaps 0;

Matches 525; Conservative 0; Mismatches 0;

QY 1 ATGAAAAAGACACTTGGCCACACTGATTGGCTTCCTCCCGCGCGCCGCACTGGCGGAA 60

DB 143 ATGAAAAAGACACTTGGCCACACTGATTGGCTTCCTCCCGCGCGCCGCACTGGCGGAA 202

QY 61 GCGGCATCCGGCTTTTAAOGTCAAGCCGATCGGCACACGCAAAAGCCCTCAAGCTCTTTA 120

DB 203 GCGGCATCCGGCTTTTAAOGTCAAGCCGATCGGCACACGCAAAAGCCCTCAAGCTCTTTA 262

QY 121 GGTTCCTGCCAAGGGCTTCAGCCCGGCATCTCCGAGGCTACGGCATCAACGACCTCCGC 180

DB 263 GGTTCCTGCCAAGGGCTTCAGCCCGGCATCTCCGAGGCTACGGCATCAACGACCTCCGC 322

QY 181 TTTCGCGCTCGATTACACGCGCTACAAAAACTATAAGCCCCCATCCACCGGATTTCAAACTT 240

DB 323 TTTCGCGCTCGATTACACGCGCTACAAAAACTATAAGCCCCCATCCACCGGATTTCAAACTT 382

QY 241 TACAGCATCGCGCGTTCGCCATTATTCGACTTCGACACCCCAATCGCCCTCAAAACGGTAT 300

DB 383 TACAGCATCGCGCGTTCGCCATTATTCGACTTCGACACCCCAATCGCCCTCAAAACGGTAT 442

QY 301 CTCGGCGCGCTTCGAGCCTCAACCGCGCTCCGTCGACTGGCGGCGAGCAGCTTC 360

DB 443 CTCGGCGCGCTTCGAGCCTCAACCGCGCTCCGTCGACTGGCGGCGAGCAGCTTC 502

QY 361 AGCCAAACCTCCATCGGCCTCGCGCTATTGACGGGCGTAAGCTATGCCGCTTACCCCGAAT 420

DB 503 AGCCAAACCTCCATCGGCCTCGCGCTATTGACGGGCGTAAGCTATGCCGCTTACCCCGAAT 562

QY 421 GTCGATTTGGATGCGCGGTACCGCTACAACTACATCGGCAAAAGTCAACTGTCAAAAAC 480

DB 563 GTCGATTTGGATGCGCGGTACCGCTACAACTACATCGGCAAAAGTCAACTGTCAAAAAC 622

QY 481 GTCGCTTCGGGGAAGTGTCCGTCGGCGTGCGGTCGAATTCGA 525

DB 623 GTCCGTTCCGGCAAGTGTCCGTCGGCGTGCGGTCGAATTCGA 667

RESULT 5

ADF4315

ID ADF4315 standard; DNA; 830 BP.

XX AC ADF4315;

XX DT 12-FEB-2004 (first entry)

XX DE N. meningitidis lipopolysaccharide DNA seq id 35.

XX KW receptor; lipid-based tumour associated antigen; cytostatic;

XX KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;

XX KW infectious disease; lipopolysaccharide; LPS; ds.

XX OS Neisseria meningitidis.

XX PN US2003157113-A1.

XX PD 21-AUG-2003.

XX PF 28-DEC-2000; 2000US-00751708.

XX PR 28-DEC-1999; 99US-0173371P.

XX PA (TERM/) TERMAN D S.

XX PI Terman DS;

XX DR WPI; 2003-787326/74.

DR P-PSDB; ADF43316.

XX New receptor in a mammalian cell that inhibits regular activation by
PT receptors specific for lipid-based tumor associated antigens, useful for
PT treating a neoplastic disease or tumor, and infectious diseases.

XX Disclosure; SEQ ID NO 35; 151pp; English.

XX The invention describes a receptor in a mammalian cell that inhibits
CC regular activation by receptors specific for lipid-based tumour
CC associated antigen. The receptor has cytostatic and antimicrobial
CC properties and is suitable for use in gene therapy. The receptors,
CC methods and compositions are useful for treating a neoplastic disease or
CC tumour (cancer), and infectious diseases. This sequence encodes Neisseria
CC meningitidis lipopolysaccharide (LPS) to which tumour cells develop
XX immunity.

SQ Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 10; Length 830;

Best Local Similarity 100.0%; Pred. No. 5.3e-125;

Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCATTGCCACACTGATTCCTCTCGCTCTCCGGCGCGCACTGGCGAA 60

DB 143 ATGAAAAAGCATTGCCACACTGATTCCTCTCGCTCTCCGGCGCGCACTGGCGAA 202

QY 61 GCGCATCCGGCTTTACGTCCAGCCGATCGGCACACGCAAAAGCCTCAAGCTCTTTA 120

DB 203 GCGCATCCGGCTTTACGTCCAGCCGATCGGCACACGCAAAAGCCTCAAGCTCTTTA 262

QY 121 GGTCTGCAAAAGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 180

DB 263 GGTCTGCAAAAGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 322

QY 181 TTGCGCGTCGATTACCGGCTACAAAACCTATAAAGCCCATCCACGATTTCAACTT 240

DB 323 TTGCGCGTCGATTACCGGCTACAAAACCTATAAAGCCCATCCACGATTTCAACTT 382

QY 241 TACAGCATCGCGCTCGCGCATTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 300

DB 383 TACAGCATCGCGCTCGCGCATTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 442

QY 301 CTCGCGCGCGCTTCAGCGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGACAGCTTC 360

DB 443 CTCGCGCGCGCTTCAGCGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGACAGCTTC 502

QY 361 AGCCAAACCTCATCGGCTCGGGGTATTGACGGGGGTAAAGCTATGCGGTTACCCCGAAT 420

DB 503 AGCCAAACCTCATCGGCTCGGGGTATTGACGGGGGTAAAGCTATGCGGTTACCCCGAAT 562

QY 421 GTCCGTTTCGGGGAACCTGTCGCTCGCGGTGCGGTCGAAATTTCTGA 525

DB 563 GTCCGTTTCGGGGAACCTGTCGCTCGCGGTGCGGTCGAAATTTCTGA 622

QY 481 GTCCGTTTCGGGGAACCTGTCGCTCGCGGTGCGGTCGAAATTTCTGA 525

DB 623 GTCCGTTTCGGGGAACCTGTCGCTCGCGGTGCGGTCGAAATTTCTGA 667

RESULT 6

Continuation (15 of 15) of AAA81490 from base 1400001 (N. meningitidis B full length gen

WP Sequence split into 15 fragments LOCUS AAA81490 Accession AAA81490

WP Fragment Name Begin End

WP AAA81490_00 1 110000

WP AAA81490_01 100001 210000

WP AAA81490_02 200001 310000

WP AAA81490_03 300001 410000

WP AAA81490_04 400001 510000

WP AAA81490_05 500001 610000

WP AAA81490_06 600001 710000

WP AAA81490_07 700001 810000

Query Match

Best Local Similarity 99.4%; Score 521.8; DB 3; Length 110000;

Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

WP AAA81490_08 800001 910000

WP AAA81490_09 900001 1010000

WP AAA81490_10 100001 1110000

WP AAA81490_11 110001 1210000

WP AAA81490_12 120001 1310000

WP AAA81490_13 130001 1410000

WP AAA81490_14 140001 1437668

Query Match 99.4%; Score 521.8; DB 3; Length 37668;

Best Local Similarity 99.6%; Pred. No. 8.4e-124;

Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCATTGCCACACTGATTCCTCTCGCTCTCCGGCGCGCACTGGCGAA 60

DB 20578 ATGAAAAAGCATTGCCACACTGATTCCTCTCGCTCTCCGGCGCGCACTGGCGAA 20519

QY 61 GCGCATCCGGCTTTACGTCCAGCCGATCGGCACACGCAAAAGCCTCAAGCTCTTTA 120

DB 20518 GCGCATCCGGCTTTACGTCCAGCCGATCGGCACACGCAAAAGCCTCAAGCTCTTTA 20459

QY 121 GGTCTGCAAAAGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 180

DB 20458 GGTCTGCAAAAGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 20399

QY 181 TTGCGCGTCGATTACAGCGCTACAAAACCTATAAAGCCCATCCACGATTTCAACTT 240

DB 20398 TTGCGCGTCGATTACAGCGCTACAAAACCTATAAAGCCCATCCACGATTTCAACTT 20339

QY 241 TACAGCATCGCGCTCGCGCATTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 300

DB 20338 TACAGCATCGCGCTCGCGCATTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 20279

QY 301 CTCGCGCGCGCTTCAGCGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGACAGCTTC 360

DB 20278 CTCGCGCGCGCTTCAGCGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGACAGCTTC 20219

QY 361 AGCCAAACCTCATCGGCTCGGGGTATTGACGGGGGTAAAGCTATGCGGTTACCCCGAAT 420

DB 20218 AGCCAAACCTCATCGGCTCGGGGTATTGACGGGGGTAAAGCTATGCGGTTACCCCGAAT 20159

QY 421 GTCCGTTTCGGGGAACCTGTCGCTCGCGGTGCGGTCGAAATTTCTGA 525

DB 20158 GTCCGTTTCGGGGAACCTGTCGCTCGCGGTGCGGTCGAAATTTCTGA 20054

RESULT 7

Continuation (7 of 15) of AAA81490 from base 600001 (N. meningitidis B full length genome

WP Sequence split into 15 fragments LOCUS AAA81490 Accession AAA81490

WP Fragment Name Begin End

WP AAA81490_00 1 110000

WP AAA81490_01 100001 210000

WP AAA81490_02 200001 310000

WP AAA81490_03 300001 410000

WP AAA81490_04 400001 510000

WP AAA81490_05 500001 610000

WP AAA81490_06 600001 710000

WP AAA81490_07 700001 810000

WP AAA81490_08 800001 910000

WP AAA81490_09 900001 1010000

WP AAA81490_10 100001 1110000

WP AAA81490_11 110001 1210000

WP AAA81490_12 120001 1310000

WP AAA81490_13 130001 1410000

WP AAA81490_14 140001 1437668

Query Match

Best Local Similarity 99.6%; Score 521.8; DB 3; Length 110000;

Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGAAAAAGCACTTCCACACATGATTGCCCTCGCTCTCCGCGCCGCGCACTGGCGGAA	60
Db	90785	ATGAAAAAGCACTTCCACACATGATTGCCCTCGCTCTCCGCGCCGCGCACTGGCGGAA	90726
QY	61	GGGCGATCCGGCTTTTACGTCGAAGCGCATGCGCGACAGCGAAAGCCCTCAAGCTCTTTA	120
Db	90725	GGGCGATCCGGCTTTTACGTCGAAGCGCATGCGCGACAGCGAAAGCCCTCAAGCTCTTTA	90666
QY	121	GGTTCTGCGCAAGGCTTACGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	180
Db	90665	GGTTCTGCGCAAGGCTTACGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	90606
QY	181	TTCCGCGTTCGATTACACGCGCTTACAAAACTATAAAGCCCATCCACCGATTTCAAACTT	240
Db	90605	TTCCGCGTTCGATTACACGCGCTTACAAAACTATAAAGCCCATCCACCGATTTCAAACTT	90546
QY	241	TACAGATCGCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAACCGTAT	300
Db	90545	TACAGATCGCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAACCGTAT	90486
QY	301	CTCGCGCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAACCGTAT	360
Db	90485	CTCGCGCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAACCGTAT	90426
QY	361	AGCCAAACCTCCATCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAAC	420
Db	90425	AGCCAAACCTCCATCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAAC	90366
QY	421	GTGATTTGGATGCGCGGTACCGCTTACAACTACATCGCGCAAGTCAACACTGTCAAAAC	480
Db	90365	GTGATTTGGATGCGCGGTACCGCTTACAACTACATCGCGCAAGTCAACACTGTCAAAAC	90305
QY	481	GTCCGTTCCGGCGAACTGTCCGTCGCGCTGCGGTCGCAAACTCTGA	525
Db	90305	GTCCGTTCCGGCGAACTGTCCGTCGCGCTGCGGTCGCAAACTCTGA	90261
RESULT 8			
AAAF21608/c			
ID	AAAF21608 standard; DNA; 349980 BP.		
AC	AAAF21608;		
DT	13-MAR-2001 (first entry)		
DE	Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.		
KW	Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;		
KW	diagnosis; antigen; detection; infection; gene therapy; antibacterial;		
OS	Neisseria meningitidis.		
PN	WO200066791-A1.		
PD	09-NOV-2000.		
XX	08-MAR-2000; 2000WO-US0005928.		
XX	30-APR-1999; 99US-0132068P.		
PR	08-OCT-1999; 99WO-US023573.		
PR	28-FEB-2000; 2000GB-00004695.		
XX	(CHIR) CHIRON CORP.		
PA	(GENO-) INST GENOMIC RES.		
XX	Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;		
PI	Massignani V, Galeotti C, Mora M, Ratti G, Scarselli M,		
PI	Rappuoli R, Frazer CW, Grandi G;		
DR	WPI; 2000-647603/62.		
XX			

PT	Neisseria meningitidis B full length genome sequence and open reading		
PT	frames are used to detect, treat and prevent Neisserial infections.		
XX			
PS	Claim 7; Appendix A; 692pp; English.		
XX			
CC	The present invention describes the full length genome of Neisseria		
CC	meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613		
CC	represent fragments of the NMB genomic sequence, as the sequence was too		
CC	long to go in a record on its own it was split into 8 sequences which		
CC	overlap each other at the beginning and end of each sequence by 49980 bp		
CC	(i.e. the last 49980 bp of AAF21544 is repeated at the beginning of		
CC	AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of		
CC	AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins		
CC	given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR		
CC	primers which are used in the exemplification of the present invention.		
CC	The NMB genome and fragments from it have antibacterial activity, and can		
CC	be used in vaccines and gene therapy. Neisseria nucleic acids, proteins		
CC	and/or antibodies which binds to the proteins can be used in compositions		
CC	for treating or preventing infection due to Neisserial bacteria or as a		
CC	diagnostic reagent for detecting the presence of Neisserial bacteria or		
CC	of antibodies raised to Neisserial bacteria. Computers, computer memory,		
CC	computer storage medium or computer databases can be used in a search to		
CC	identify open reading frames (ORFs) or coding sequences within the NMB		
CC	genome. The DNA sequences provide further opportunities to find antigenic		
CC	or immunogenic proteins which are more effective in vaccines than the		
CC	outer membrane proteins currently used		
XX			
SQ	Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 U; 0 Other;		
	Query Match	99.4%;	Score 521.8; DB 3; Length 349980;
	Best Local Similarity	99.6%;	Pred. No. 1.4e-123;
	Matches 523;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
QY	1	ATGAAAAAGCACTTCCACACATGATTGCCCTCGCTCTCCGCGCCGCGCACTGGCGGAA	60
Db	90786	ATGAAAAAGCACTTCCACACATGATTGCCCTCGCTCTCCGCGCCGCGCACTGGCGGAA	90727
QY	61	GGCGCATCCGGCTTTTACGTCGAAGCGCATGCGCGACAGCGAAAGCCCTCAAGCTCTTTA	120
Db	90726	GGCGCATCCGGCTTTTACGTCGAAGCGCATGCGCGACAGCGAAAGCCCTCAAGCTCTTTA	90667
QY	121	GGTTCTGCGCAAGGCTTACGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	180
Db	90666	GGTTCTGCGCAAGGCTTACGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	90607
QY	181	TTCCGCGTTCGATTACACGCGCTTACAAAACTATAAAGCCCATCCACCGATTTCAAACCT	240
Db	90606	TTCCGCGTTCGATTACACGCGCTTACAAAACTATAAAGCCCATCCACCGATTTCAAACCT	90547
QY	241	TACAGATCGCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAACCGTAT	300
Db	90546	TACAGATCGCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAACCGTAT	90487
QY	301	CTCGCGCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAACCGTAT	360
Db	90486	CTCGCGCGCGCTTCGCGCATTTAGACTTCGACACCCCAATCGCCGTCGCAACCGTAT	90427
QY	361	AGCCAAACCTCCATCGCGCTTCGCGCATTTAGCGCGCGTAAAGCTATGTCGCGTTACCCCGAAT	420
Db	90426	AGCCAAACCTCCATCGCGCTTCGCGCATTTAGCGCGCGTAAAGCTATGTCGCGTTACCCCGAAT	90367
QY	421	GTGCGATTTGGATGCGCGGTACCGCTTACAACTACATCGGCAAGTCAACACTGTCAAAAAC	480
Db	90366	GTGCGATTTGGATGCGCGGTACCGCTTACAACTACATCGGCAAGTCAACACTGTCAAAAAC	90307
QY	481	GTCCGTTCCGGCGAACTGTCCGTCGCGGTGCGCGTCAAAATTCCTGA	525
Db	90306	GTCCGTTCCGGCGAACTGTCCGTCGCGGTGCGCGTCAAAATTCCTGA	90262
RESULT 9			
AAT39041			
ID	AAT39041 standard; DNA; 850 BP.		

XX AC AAT39041;
 XX 16-OCT-2003 (revised)
 DT 22-DEC-1996 (first entry)
 XX DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
 KW antibody; detection; probe; surface protein; ss.
 XX OS Neisseria meningitidis; strain Z4063.
 XX FT Key Location/Qualifiers
 FT CDS 208..732 /*tag= a
 FT sig_peptide 208..264 /*tag= b
 FT mat_peptide 265..729 /*tag= c
 XX PN W09629412-A1.
 XX PD 26-SEP-1996.
 XX PF 15-MAR-1996; 96WO-CA000157.
 XX PR 17-MAR-1995; 95US-00406362.
 PR 04-AUG-1995; 95US-0001983P.
 XX PA (IAFB-) IAF BIO VAC INC.
 XX PI Brodeur BR, Martin D, Hamel J, Rioux C;
 XX WPI; 1996-443187/44.
 DR P-PSDB; AAW04893.
 XX NEisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against, or
 PT diagnosis of, N. meningitidis infection.
 XX Claim 12; Fig 9; 117pp; English.
 XX A proteinase K resistant surface protein has been isolated from 4 strains
 CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
 CC antigenic fragments of antibodies can be used in a vaccine for the
 CC prevention of infection by N. meningitidis or by N. gonorrhoeae in
 CC humans. The antibodies may also be used diagnostically to detect N.
 CC meningitidis infection. The antigen may also be used to detect antibodies
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,
 CC or their fragments, can be used as probes for the detection of pathogenic
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
 XX Sequence 850 BP; 208 A; 273 C; 185 G; 184 T; 0 U; 0 Other;
 SQ Query Match 98.8%; Score 518.6; DB 2; Length 850;
 Best Local Similarity 99.2%; Pred. No. 2.3e-123;
 Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ATGAAAAGCACTGCGACACTGATTCCTCGCTCTCCGCGCGCGGCGGCGGAA 60
 DB 208 ATGAAAAGCACTGCGACACTGATTCCTCGCTCTCCGCGCGCGGCGGCGGAA 267
 QY 61 GCGCATCGGCTTTTACGTCCAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
 DB 268 GCGCATCGGCTTTTACGTCCAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 327
 QY 121 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 180
 DB 328 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 387
 QY 181 TTCGCGTCGATTACACGGCTACAAAACCTATAAGCCCATCCACCGATTCAACTT 240

Db 388 TTCGCCGTGATTACACGGCTACAAAACCTATAAGCCCATCCACGGATTTCAAACTT 447
 QY 241 TACAGCATCGGCGGTCCGCCATTTAGCACTTCGACACACCCCAATCGCCGTCACACCGTAT 300
 Db 448 TACAGCATCGGCGGTCCGCCATTTAGCACTTCGACACACCCCAATCGCCGTCACACCGTAT 507
 QY 301 CTGCGCGCGGCTTGAAGCTCAACCGGCTCCCTCGACTTGGGCGGAGGACAGCTTC 360
 Db 508 CTGCGCGCGGCTTGAAGCTCAACCGGCTCCCTCGACTTGGGCGGAGGACAGCTTC 567
 QY 361 AGCCAAACCTCCATCGGCTCGGCTATTGACGGGCTTAAGCTATGCCGTTACCCCGAAT 420
 Db 568 AGCCAAACCTCCATCGGCTCGGCTATTGACGGGCTTAAGCTATGCCGTTACCCCGAAT 627
 QY 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
 Db 628 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 687
 QY 481 GTCGTTCCGGCGAAGTGTGCGTGGGCTGCGGCTGCGGCTCAAAATTTCTGA 525
 Db 688 GTCGTTCCGGCGAAGTGTGCGGCTGCGGCTGCGGCTCAAAATTTCTGA 732
 RESULT 10
 ABS67381
 ID ABS67381 standard; DNA; 710 BP.
 XX AC ABS67381;
 XX DT 29-NOV-2002 (first entry)
 XX DE Neisseria gonorrhoeae outer membrane gene #1.
 XX KW Gram-negative bacterial bleb; PorB; outer membrane protein;
 KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
 KW protective antigen; antibacterial; vaccine; gene; ds.
 XX OS Neisseria gonorrhoeae.
 XX PN W0200262380-A2.
 XX PD 15-AUG-2002.
 XX PF 08-FEB-2002; 2002WO-EP001356.
 XX PR 08-FEB-2001; 2001GB-00003169.
 XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;
 XX WPI; 2002-657510/70.
 DR P-PSDB; ABG91063.
 XX Novel gram-negative bacterial bleb presenting on its surface PorB outer
 PT membrane protein from Chlamydia trachomatis or protective antigen from
 PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.
 XX Disclosure; Page 54; 75pp; English.
 XX The present invention relates to a new gram-negative bacterial bleb
 CC presenting on its surface the PorB outer membrane protein from Chlamydia
 CC trachomatis, or a protective antigen from C. pneumoniae. The invention is
 CC useful for preventing C. trachomatis or C. pneumoniae infection in a
 CC host. The present nucleic acid sequence represents a Neisseria
 CC gonorrhoeae gene as described in the invention
 XX SQ Sequence 710 BP; 171 A; 228 C; 160 G; 151 T; 0 U; 0 Other;
 Query Match 95.7%; Score 502.6; DB 6; Length 710;
 Best Local Similarity 97.3%; Pred. No. 2.9e-119;
 Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGCACACGATGTCCTCGCTCTCCCGCGCGCGCACTGGCGAA 60
 DB 141 ATGAAAAAGCACTTGCACACGATGTCCTCGCTCTCCCGCGCGCGCACTGGCGAA 200
 QY 61 GCGCATCCGGCTTTTACGTCGACGCGATGCGCACAGCAAAAGCTTCAAGCTCTTTA 120
 DB 201 GCGCATCCGGCTTTTACGTCGACGCGATGCGCACAGCAAAAGCTTCAAGCTCTTTA 260
 QY 121 GGTTCGCAAGGCTTCAAGCGCGCATCTCGGAGGCTACCGCATCAACGACCTCCGC 180
 DB 261 GGTTCGCAAGGCTTCAAGCGCGCATCTCGGAGGCTACCGCATCAACGACCTCCGC 320
 QY 181 TTTCGCGTTCGATACACGCGCTTCAAAAACTATAAGCCCGCATCCACGATTTCAAACCT 240
 DB 321 TTTCGCGTTCGATACACGCGCTTCAAAAACTATAAGCCCGCATCCACGATTTCAAACCT 380
 QY 241 TACAGCATCCGGCGTTCGCGCTTTTACGATTCGACACCCCAATCGCGCGTCAAAACCGTAT 300
 DB 381 TACAGCATCCGGCGTTCGCGCTTTTACGATTCGACACCCCAATCGCGCGTCAAAACCGTAT 440
 QY 301 CTCGCGCGCGCTTACGCGCTCAACCGCGCTCGCTCGACTTGGGGGCGAGCGACGCTTC 360
 DB 441 TTCGCGCGCGCTTACGCGCTCAACCGCGCTTCGCGCGCTTGGGGGCGAGCGACGCTTC 500
 QY 361 AGCCAAACCTCCATCGCGCTCGCGCTTATGACGGGCTAAGCTATGCGGTTACCCCGAAT 420
 DB 501 AGCCAAACCTCCGCGCGCTCGCGCTTATGACGGGCTAAGCTATGCGGTTACCCCGAAT 560
 QY 421 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAAAGTCAAGACTGTCAAAAC 480
 DB 561 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAAAGTCAAGACTGTCAAAAC 620
 QY 481 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAAAGTCAAAATTTCTGA 525
 DB 621 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAAAGTCAAAATTTCTGA 665

RESULT 11

AAT39042
 ID AAT39042 standard; DNA; 810 BP.

AC AAT39042;

DT 16-OCT-2003 (revised)

DT 22-DEC-1996 (first entry)

DE Proteinase K resistant N. meningitidis 22 kD surface protein.

XX Proteinase K resistant; *Neisseria meningitidis*; *Neisseria gonorrhoeae*;

KW antibody; detection; probe; surface protein; ss.

OS *Neisseria meningitidis*; strain b2.

FH Key Location/Qualifiers

FT CDS 241..765

FT /*tag= a

FT sig_peptide 241..297

FT /*tag= b

FT sig_peptide 298..762

FT /*tag= c

XX WO9629412-A1.

XX 26-SEP-1996.

XX 15-MAR-1996; 96WO-CA000157.

XX 17-MAR-1995; 95US-00406362.

XX 04-AUG-1995; 95US-0001983P.

XX (IAFB-) IAF BIO VAC INC.

XX Brodeur BR, Martin D, Hamel J, Rioux C;

PI

XX WPI; 1996-443187/44.
 DR P-PSDB; AAW04894.
 XX *Neisseria meningitidis* antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against, or
 PT diagnosis of, *N. meningitidis* infection.
 XX Claim 12; Fig 10; 117pp; English.
 PS A proteinase K resistant surface protein has been isolated from 4 strains
 CC of *N. meningitidis* (AAT39039 to AAT39042). The isolated 22 kD antigen,
 CC antigenic fragments of antibodies can be used in a vaccine for the
 CC prevention of infection by *N. meningitidis* or by *N. gonorrhoeae* in
 CC humans. The antibodies may also be used diagnostically to detect *N.*
 CC *meningitidis* infection. The antigen may also be used to detect antibodies
 CC specific to *N. meningitidis* antigen. DNA sequences encoding the antigen,
 CC or their fragments, can be used as probes for the detection of pathogenic
 CC *Neisseria* bacteria. (Updated on 16-OCT-2003 to standardise OS field)
 XX Sequence 810 BP; 186 A; 260 C; 186 G; 178 T; 0 U; 0 Other;

Query Match 95.7%; Score 502.6; DB 2; Length 810;

Best Local Similarity 97.3%; Pred. No. 36-119;

Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGCACACGATGTCCTCGCTCTCCCGCGCGCGCACTGGCGAA 60

DB 241 ATGAAAAAGCACTTGCACACGATGTCCTCGCTCTCCCGCGCGCGCACTGGCGAA 300

QY 61 GCGCATCCGGCTTTTACGTCGACGCGATGCGCACAGCAAAAGCTTCAAGCTCTTTA 120

DB 301 GCGCATCCGGCTTTTACGTCGACGCGATGCGCACAGCAAAAGCTTCAAGCTCTTTA 360

QY 121 GGTTCGCAAGGCTTCAAGCGCGCATCTCGGAGGCTACCGCATCAACGACCTCCGC 180

DB 361 GGTTCGCAAGGCTTCAAGCGCGCATCTCGGAGGCTACCGCATCAACGACCTCCGC 420

QY 181 TTTCGCGTTCGATACACGCGCTACAAAACTATAAGCCCGCATCCACGATTTCAAACCT 240

DB 421 TTTCGCGTTCGATACACGCGCTACAAAACTATAAGCCCGCATCCACGATTTCAAACCT 480

QY 241 TACAGCATCCGGCGTTCGCGCTTACGATTCGACACCCCAATCGCGCGTCAAAACCGTAT 300

DB 481 TACAGCATCCGGCGTTCGCGCTTACGATTCGACACCCCAATCGCGCGTCAAAACCGTAT 540

QY 301 CTCGCGCGCGCTTACGCGCTCAACCGCGCTCCGTCGACTTGGGGGCGAGCGACGCTTC 360

DB 541 TTCGCGCGCGCTTACGCGCTCAACCGCGCTTCGCGCGCTTGGGGGCGAGCGACGCTTC 600

QY 361 AGCCAAACCTCCATCCGCGCTCGCGCTTATGACGGGCTAAGCTATGCGGTTACCCCGAAT 420

DB 601 AGCCAAACCTCCGCGCGCTCGCGCTTATGACGGGCTAAGCTATGCGGTTACCCCGAAT 660

QY 421 GTCGATTTGGATGCGCGCTACCGCTACAACTACGCGCAAAAGTCAAGACTGTCAAAAC 480

DB 661 GTCGATTTGGATGCGCGCTACCGCTACAACTACGCGCAAAAGTCAAGACTGTCAAAAC 720

QY 481 GTCGATTTGGATGCGCGCTACCGCTACAACTACGCGCAAAAGTCAAAATTTCTGA 525

DB 721 GTCGATTTGGATGCGCGCTACCGCTACAACTACGCGCAAAAGTCAAAATTTCTGA 765

RESULT 12

AAT39040

ID AAT39040 standard; DNA; 710 BP.

XX AAT39040;

AC AAT39040;

XX 16-OCT-2003 (revised)

DT 22-DEC-1996 (first entry)

XX Proteinase K resistant *N. meningitidis* 22 kD surface protein.

DE

```

XX KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
XX antibody; detection; probe; surface protein; ss.
XX OS Neisseria meningitidis; strain MCH88.
XX FH Key Location/Qualifiers
FT CDS 116..643
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c
XX PN W09629412-A1.
XX PD 26-SEP-1996.
XX PF 15-MAR-1996; 96WO-CA000157.
XX PR 17-MAR-1995; 95US-00406362.
XX PR 04-AUG-1995; 95US-0001983P.
XX PA (IAFB-) IAF BIO VAC INC.
XX PI Brodeur BR, Martin D, Hamel J, Rioux C;
XX WPI; 1996-443187/44.
XX P-PSDB; AAW04892.
XX Neisseria meningitidis antigen, highly conserved between different
XX strains - useful for prodn. of antibodies for immunisation against, or
XX diagnosis of, N. meningitidis infection.
XX Claim 12; Fig 8; 117pp; English.
XX A proteinase K resistant surface protein has been isolated from 4 strains
XX of N. meningitidis (AAR39039 to AAT39042). The isolated 22 kD antigen,
XX antigenic fragments of antibodies can be used in a vaccine for the
XX prevention of infection by N. meningitidis or by N. gonorrhoeae in
XX humans. The antibodies may also be used diagnostically to detect N.
XX meningitidis infection. The antigen may also be used to detect antibodies
XX specific to N. meningitidis antigen. DNA sequences encoding the antigen,
XX or their fragments, can be used as probes for the detection of pathogenic
XX Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
XX Sequence 710 BP; 174 A; 232 C; 148 G; 156 T; 0 U; 0 Other;

Query Match 93.6%; Score 491.2; DB 2; Length 710;
Best Local Similarity 97.0%; Pred. No. 2.5e-116;
Matches 512; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

QY 1 ATGAAAAGCACTTGCACACTGATTCCTCGCTCTCCGGCGCGCACTGCGGAA 60
DB 116 ATGAAAAGCACTTGCACACTGATTCCTCGCTCTCCGGCGCGCACTGCGGAA 175
QY 61 GCGCATCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
DB 176 GCGCATCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 235
QY 121 GGTTCGCAAAAGCTTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGACCTCCGC 180
DB 236 GGTTCGCAAAAGCTTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGACCTCCGC 295
QY 181 TTCGCGCTCGATTACACGGCTTACAAAACATA---AAGCCCATCCACCGATTCAA 237
DB 296 TTCGCGCTCGATTACACGGCTTACAAAACATA---AAGCCCATCCACCGATTCAA 355
QY 238 CTTTACAGCATCGGCGCTCGCCATTTACGACTTCGACACCAATCGCCGTCAAACCG 297
DB 356 CTTTACAGCATCGGCGCTCGCCATTTACGACTTCGACACCAATCGCCGTCAAACCG 415
QY 298 TATCTCGGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGGCGGACGACAGC 357

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Db 416 TATCTCGGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTTAACGGCAGCAGC 475
QY 358 TTACGCCAAACCTCCATCGGCTTATGACGGCGGTAAGCTATGCGGTTACCCCG 417
DB 476 TTACGCCAAACCTCCATCGGCTTATGACGGCGGTAAGCTATGCGGTTACCCCG 535
QY 418 AATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACTGTCAA 477
DB 536 AATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACTGTCAA 595
QY 478 AACGTCGCTTCCGGGAACTGTGCTGCGGCTGCGGCTCAAAATCTGA 525
DB 596 AATGTCGCTTCCGGGAACTGTGCTGCGGCTGCGGCTCAAAATCTGA 643

RESULT 13
ABZ38961
ID ABZ38961 standard; DNA; 525 BP.
XX AC ABZ38961;
XX DT 07-MAR-2003 (first entry)
XX DE N. gonorrhoeae nucleotide sequence SEQ ID 2511.
XX KW Antibacterial; infection; vaccine; gene therapy; gene; ds.
XX OS Neisseria gonorrhoeae.
XX FN W0200279243-A2.
XX PD 10-OCT-2002.
XX PF 12-FEB-2002; 2002WO-1B002069.
XX PR 12-FEB-2001; 2001GB-00003424.
XX PA (CHIR-) CHIRON SPA.
XX PI Fontana MR, Pizza M, Massignani V, Monaci E;
XX WPI; 2003-058415/05.
XX P-PSDB; ABP77991.
XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
XX medicament for treating or preventing N. gonorrhoeae infection.
XX Disclosure; Page 371; 815pp; English.
XX The present invention relates to proteins from Neisseria gonorrhoeae.
XX Also disclosed are the nucleic acid molecules encoding the proteins and
XX antibodies that specifically bind to the proteins. The composition
XX comprising the protein, nucleic acid or antibody is useful for the
XX manufacture of a medicament for treating or preventing N. gonorrhoeae
XX infection, this may be in the form of a vaccine or gene therapy.
XX Sequences given in records ABZ37706-ABZ42016 represent nucleic acid
XX molecules of the invention
XX Sequence 525 BP; 117 A; 188 C; 120 G; 100 T; 0 U; 0 Other;

Query Match 91.5%; Score 480.2; DB 10; Length 525;
Best Local Similarity 96.0%; Pred. No. 1.5e-113;
Matches 504; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

QY 1 ATGAAAAGCACTTGCACACTGATTCCTCGCTCTCCGGCGCGCACTGCGGAA 60
DB 1 ATGAAAAGCACTTGCACACTGATTCCTCGCTCTCCGGCGCGCACTGCGGAA 60
QY 61 GCGCATCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
DB 61 GCGCATCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120

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QY 121 GGTTCGCCAAGGCTTACAGCCGCGCATCTCGCAGGCTACCGCATCAACGACCTCCGC 180
 Db |||||
 121 GGTTCGCCAAGGCTTACAGCCGCGCATCTCGCAGGCTACCGCATCAACGACCTCCGC 180
 QY 181 TTCCGCGTCGATTACACGCGCTACAAAACTATA---AAGCCCAATCCACCGATTCAAA 237
 Db |||||
 181 TTCCGCGTCGATTACACGCGCTACAAAACTATA---AAGCCCAATCCACCGATTCAAA 240
 QY 238 CTTTACAGCATCGCGCGCTCGGCATTTACGACTTCGACACCAATCGCCCGTCAAAACCG 297
 Db |||||
 241 CTTTACAGCATCGCGCGCTCGGCATTTACGACTTCGACACCAATCGCCCGTCAAAACCG 300
 QY 298 TATCTCGCGCGCGCTTGAGCTCAACCGCGCTCGCTCGACTTGCGCGCGCGAGCAGACG 357
 Db |||||
 301 TATCTCGCGCGCGCTTGAGCTCAACCGCGCTCGCTCGACTTGCGCGCGCGAGCAGACG 360
 QY 358 TTCAGCAAACTCCATCGCGCTCGCGCTATTCAGCGGGGTAAAGCTATCGCGTTACCCCG 417
 Db |||||
 361 TTCAGCAAACTCCATCGCGCTCGCGCTATTCAGCGGGGTAAAGCTATCGCGTTACACCC 420
 QY 418 AATGTCGATTGGATCGCGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAA 477
 Db |||||
 421 AATGTCGATTGGATCGCGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAA 480
 QY 478 AAGTCGCTTCGCGCGAACTGTCGCGCGCTCGCGCTCGCGCTCGCGCTCGCGCTCGCG 522
 Db |||||
 481 AAGTCGCTTCGCGCGAACTGTCGCGCGCTCGCGCTCGCGCTCGCGCTCGCGCTCGCG 525

RESULT 14

ADL13425
 ID ADL13425 standard; DNA; 468 BP.
 AC ADL13425;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE *Neisseria meningitidis* H44/76 mature NspA-encoding DNA.
 XX
 KW *Neisserial* surface protein A; NspA; refolding; recombinant production;
 KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;
 KW invasive bacterial disease; bacteraemia; meningitis;
 KW *Neisseria gonorrhoeae*; gonorrhoea; mature protein; strain H44/76;
 KW antibacterial; gene therapy; gene; ds.
 XX
 OS *Neisseria meningitidis*; H44/76.

Key Location/Qualifiers
 CDS 1..468
 /tag= b
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 /product= "Mature NspA"
 /note= "No start codon given"
 mat_peptide 1..465
 /tag= a
 /product= "Mature NspA"

WO2004020452-A2.

11-MAR-2004.

28-AUG-2003; 2003WO-EP010085.

30-AUG-2002; 2002GB-00020197.

(GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
 (UYUT-) RIJKSUNIV UTRECHT.

XX Biemanns R, Bos M, Denoel P, Feron C, Goraj K, Poolman J;
 PI Tommassen J, Weynants V;
 DR WPI: 2004-239150/22.
 DR P-PSDB; ADL13426.

XX
 PT New refolded NspA protein, useful for preparing a composition for
 PT diagnosing, treating or preventing infection caused by *Neisseria*
 PT meningitidis or *Neisseria gonorrhoeae*.
 XX
 PS Example 1; Fig 2; 62pp; English.
 XX
 CC The invention relates to an isolated refolded *Neisserial* surface protein
 CC A (NspA) from *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The
 CC invention also relates to the method of refolding an NspA protein; an
 CC alkaline refolding buffer comprising ethanolamine and SB-12 (3-
 CC dimethyldecylammonioethanesulphonate) for refolding an NspA protein; a
 CC pharmaceutical composition comprising the refolded NspA protein, a
 CC carrier and optionally one or more other *Neisserial* antigens; a method of
 CC preventing or treating a *Neisserial* infection; an antibody immunospecific
 CC for the NspA protein; and diagnosing a *Neisserial* infection. NspA has
 CC characteristics which indicate that it is a potential vaccine candidate
 CC for the development of subunit vaccines for the treatment of infections
 CC caused by *Neisseria meningitidis* (meningococcus), which causes invasive
 CC bacterial diseases such as bacteraemia and meningitis, or *Neisseria*
 CC gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced
 CC NspA could therefore be used to produce vaccine compositions and it could
 CC also be used in the development of new antimicrobial agents, diagnostic
 CC tests and in drug screening. However, recombinantly produced proteins are
 CC frequently unable to adopt their biologically active conformations, and
 CC yields may be very low due to mis-folding and aggregation of the protein.
 CC The method of the invention provides an improved method for refolding the
 CC NspA protein, and it is possible to increase the recovery of active
 CC protein form partly purified inclusion bodies in amounts up to 100%
 CC without the need for further purification. The refolded NspA protein is
 CC useful for preparing a composition for diagnosing, treating or preventing
 CC infection caused by *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The
 CC present sequence represents DNA encoding the mature NspA protein from
 CC *Neisseria meningitidis* H44/76 which was amplified and cloned in an
 CC example of the invention.

Sequence 468 BP; 105 A; 164 C; 106 G; 93 T; 0 U; 0 Other;

Query Match 88.5%; Score 464.8; DB 12; Length 468;

Best Local Similarity 99.6%; Pred. No. 1.4e-109;

Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCGCATCGCGCTTTTACGTCCAAAGCGATGCCGACAGCAAGAGCTCAAGCTCT 117
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 1 GAAGCGCATCGCGCTTTTACGTCCAAAGCGATGCCGACAGCAAGAGCTCAAGCTCT 60
 QY 118 TTAGGTCTTGCACAAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAACGACCTC 177
 Db |||||
 61 TTAGGTCTTGCACAAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAACGACCTC 120
 QY 178 CGCTTCGCGCTCGATTACACGCGCTACAAAACTATAAGCCCGCATCCACCGATTCAAA 237
 Db |||||
 121 CGCTTCGCGCTCGATTACACGCGCTACAAAACTATAAGCCCGCATCCACCGATTCAAA 180
 QY 238 CTTTACAGCATCGCGCGCTCGGCATTTACGACTTCGACACCAATCGCCCGTCAAAACCG 297
 Db |||||
 181 CTTTACAGCATCGCGCGCTCGGCATTTACGACTTCGACACCAATCGCCCGTCAAAACCG 240
 QY 298 TATCTCGCGCGCGCTTGAGCGCTCAACCGCGCTCCGTCGACTTGGGGGAGCGACAGC 357
 Db |||||
 241 TATCTCGCGCGCGCTTGAGCGCTCAACCGCGCTCCGTCGACTTGGGGGAGCGACAGC 300
 QY 358 TTTACGCCAAACCTCCATCGCGCTCGCGGTATTGACGGGCGTAAGCTATGCCGTTACCCCG 417
 Db |||||
 301 TTTACGCCAAACCTCCATCGCGCTCGCGGTATTGACGGGCGTAAGCTATGCCGTTACCCCG 360
 QY 418 AATGTCGATTGGATCGCGGTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAA 477
 Db |||||
 361 AATGTCGATTGGATCGCGGTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAA 420
 QY 478 AACGTCGCTTCGCGCGAACTGTCCGCGCGGTGTCGCGCGTCAAAATTCGA 525
 Db |||||
 421 AACGTCGCTTCGCGCGAACTGTCCGCGCGGTGTCGCGCGTCAAAATTCGA 468

RESULT 15

ID ABZ38960/c

XX ABZ38960 standard; DNA; 486 BP.

XX AC ABZ38960;

XX XX 07-MAR-2003 (first entry)

XX N. gonorrhoeae nucleotide sequence SEQ ID 2509.

XX Antibacterial; infection; vaccine; gene therapy; gene; ds.

XX Neisseria gonorrhoeae.

XX WO200279243-A2.

XX PD 10-OCT-2002.

XX PF 12-FEB-2002; 2002WO-IB002069.

XX PR 12-FEB-2001; 2001GB-00003424.

XX PA (CHIR-) CHIRON SPA.

XX Fontana MR, Pizza M, Massignani V, Monaci E;

XX WPI; 2003-058415/05.

XX DR P-PSDB; ABP77990.

XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection.

XX Disclosure; Page 371; 815pp; English.

XX The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy.

XX Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention

XX SQ Sequence 486 BP; 101 A; 107 C; 168 G; 110 T; 0 U; 0 Other;

Query Match 70.1%; Score 368; DB 10; Length 486;

Best Local Similarity 95.6%; Pred. No. 1e-84;

Matches 390; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 121 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGACCTCCGC 180

DB 486 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGACCTCCGC 427

QY 181 TTCCGCGTCGATTACACGGCTACAAAACCTATA---AAGCCCATCCACCGATTTCAAA 237

DB 426 TTCCGCGTCGATTACACGGCTACAAAACCTATAAAAGCCCATCCACCGATTTCAAA 367

QY 238 CTTTACAGCATCGGCGGTTCGCCATTACGACTTCGACACCCAAATCGCCGTCAAACCG 297

DB 366 CTTTACAGCATCGGCGGTTCGCCATTACGACTTCGACACCCAAATCGCCGTCAAACCG 307

QY 298 TATCTCGGCGCGCTTCAGCCCTCAACCGCTCCGCTCGACTTGGGCGGAGGACACAGC 357

DB 306 TATTCGGCGCGCTTCAGCCCTCAACCGCTTCGCCCTCCGCGCTTGGGCGGAGGACACAGC 247

QY 358 TTCAGCCAAACCTCCATCGGCTTCGGCGTATTGACGGGTAAGCTATGCCGTTACCCCG 417

DB 246 TTCAGCCAAACCTCCATCGGCTTCGGCGTATTGACGGGTAAGCTATGCCGTTACACCC 187

QY 418 AATGTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAA 477

Db 186 AATGTCGATTGGATGCGGCTACCGCTACAACTACGTCGCAAAAGTCAACAAATGTCAA 127

Qy 478 AACGTCGTTCCGCGCAACTGTCCGTCCGCGTCCGCGTCAAAATTTCTGA 525

Db 126 AACGTCGTTCCGCGCAACTGTCCGCGCGGCGTCCGCGTCAAAATTTCTGA 79

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OM nucleic - nucleic search, using sw model

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1590.825 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525	100.0	830	3	US-08-913-362-1
2	518.6	98.8	850	3	US-08-913-362-5
3	502.6	95.7	810	3	US-08-913-362-7
4	501.2	95.5	528	3	US-08-913-362-29
5	491.2	93.6	710	3	US-08-913-362-3
6	49.8	9.5	1919	4	US-09-614-913-175
7	45.6	8.7	4403765	3	US-09-103-840A-2
8	45.6	8.7	4411529	3	US-09-103-840A-1
9	45	8.6	4403765	3	US-09-103-840A-2
10	45	8.6	4411529	3	US-09-103-840A-1
11	44	8.4	1082	4	US-09-881-165-4
12	44	8.4	4483	3	US-08-961-527-363
13	44	8.4	32768	3	US-08-961-527-71
14	43.6	8.3	390	3	US-09-197-649-7
15	43	8.2	925	3	US-08-858-003-1
16	43	8.2	925	3	US-09-078-166-1
17	43	8.2	925	3	US-08-997-467-1
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22	42	8.0	1859	3	US-08-894-818B-15
23	42	8.0	1977	3	US-08-894-818B-2
24	42	8.0	1377	3	US-08-894-818B-6
25	42	8.0	1977	3	US-09-445-472-11
26	42	8.0	1377	4	US-10-090-624-11
27	41.6	7.9	867	4	US-09-216-393B-340

28	41.6	7.9	867	4	US-09-216-393B-342	Sequence 342, App
29	41.6	7.9	1397	4	US-09-216-393B-343	Sequence 343, App
30	41.6	7.9	1397	4	US-09-216-393B-345	Sequence 345, App
31	41.4	7.9	1614	4	US-09-489-039A-3484	Sequence 3484, Ap
32	41.4	7.9	1698	4	US-09-489-039A-3505	Sequence 3505, Ap
33	41.4	7.9	1706	4	US-10-033-109-3	Sequence 3, Appli
34	41.4	7.9	3486	4	US-09-614-221A-292	Sequence 292, App
35	41.4	7.9	25254	4	US-09-902-540-1233	Sequence 1233, Ap
36	41.2	7.8	1781	4	US-09-675-018B-7	Sequence 7, Appli
37	41.2	7.8	1889	4	US-09-675-018B-9	Sequence 9, Appli
38	41	7.8	1439	3	US-09-056-556-167	Sequence 167, App
39	41	7.8	1439	3	US-09-072-596-162	Sequence 162, App
40	41	7.8	1439	3	US-09-072-967-167	Sequence 167, App
41	40.8	7.8	822	3	US-09-228-986-38	Sequence 38, Appli
42	40.8	7.8	822	4	US-10-101-464A-38	Sequence 38, Appli
43	40.8	7.8	2138	4	US-10-101-464A-462	Sequence 462, App
44	40.8	7.8	7218	1	US-08-232-463-14	Sequence 14, Appl
45	40.6	7.7	435	4	US-09-252-991A-6817	Sequence 6817, Ap

ALIGNMENTS

RESULT 1
US-08-913-362-1
; Sequence 1, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001.983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 830 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 143..667
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 143..199
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 200..667
; US-08-913-362-1

Query Match      100.0%; Score 525; DB 3; Length 830;
Best Local Similarity 100.0%; Pred. No. 4.8e-138;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGCACACTGATTGGCTTCCCGCCCGCGCACTTGGCGGAA 60
Db 143 ATGAAAAAGCACTTGCACACTGATTGGCTTCCCGCCCGCGCACTTGGCGGAA 202

QY 61 GCGGCATCCGGCTTTTACGTCCTCAGCGGATGCGGCACACGCAAAAGCCTCAAGCTCTTTA 120
Db 203 GCGGCATCCGGCTTTTACGTCCTCAGCGGATGCGGCACACGCAAAAGCCTCAAGCTCTTTA 262

QY 121 GGTTCGCCAAAGGCTTACGCCCGCGCATCTCCGAGGCTTACCGCATCAACGACCTCCGC 180
Db 263 GGTTCGCCAAAGGCTTACGCCCGCGCATCTCCGAGGCTTACCGCATCAACGACCTCCGC 322

QY 181 TTCCGCGTGCATTACAGCGCTCAAAAACTATAAAGCCCATCCACCGATTTCAAACTT 240
Db 323 TTCCGCGTGCATTACAGCGCTCAAAAACTATAAAGCCCATCCACCGATTTCAAACTT 382

QY 241 TACAGCATCGCGCGTCCGCTTACGACTTTCAGCTTTCGACACCCCAATCGCCGTCGCAACCGTAT 300
Db 383 TACAGCATCGCGCGTCCGCTTACGACTTTCAGCTTTCGACACCCCAATCGCCGTCGCAACCGTAT 442

QY 301 CTCGGCGCGGCTTGAGCCTCAACCGCGCTCGCTCGATTTGGCGGCGGACGACGCTTC 360
Db 443 CTCGGCGCGGCTTGAGCCTCAACCGCGCTCGCTCGATTTGGCGGCGGACGACGCTTC 502

QY 361 AGCCTAACCTCATCGGCTTCCGCTTATTCAGCGGCGTGAAGCTATCGGCTTACCCCGAAT 420
Db 503 AGCCTAACCTCATCGGCTTCCGCTTATTCAGCGGCGTGAAGCTATCGGCTTACCCCGAAT 562

QY 421 GTCGATTGTGATCCCGCTACCGCTACAACTACATCGCAAAAGTCAACACTGTCAAAAAC 480
Db 563 GTCGATTGTGATCCCGCTACCGCTACAACTACATCGCAAAAGTCAACACTGTCAAAAAC 622

QY 481 GTCGTTCCGGGGAAGTGTCCGTCGCGTCCGCTCAAAATTCGTA 525
Db 623 GTCGTTCCGGGGAAGTGTCCGTCGCGTCCGCTCAAAATTCGTA 667

RESULT 2
US-08-913-362-5
; Sequence 5, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

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Qy 361 AGCAAACTCCATCGGCTCGGCTATGTGACGGCGTAACTATGCGTTACCCGAAT 420
Db 568 AGCAAACTCCATCGGCTCGGCTATGTGACGGCGTAACTATGCGTTACCCGAAT 627
Qy 421 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
Db 628 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 687
Qy 481 GTCGTTCCGCGAACTGTCGCTCGGCTGGCGGTCAAAATCTGA 525
Db 688 GTCGTTCCGCGAACTGTCGCTCGGCTGGCGGTCAAAATCTGA 732

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RESULT 3
US-08-913-362-7
; Sequence 7, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 810 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria gonorrhoeae
; STRAIN: b2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 241..765
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 241..297

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; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 298..765
; US-08-913-362-7
;
; Query Match 95.7%; Score 502.6; DB 3; Length 810;
; Best Local Similarity 97.3%; Pred. No. 9.5e-132; Indels 0; Gaps 0;
; Matches 511; Conservative 0; Mismatches 14;
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Qy 1 ATGAAAAAGCACTTGCACACTGATTCCTCTCCCGCGCGCGACGTCGCGAA 60
Db 241 ATGAAAAAGCACTTGCACACTGATTCCTCTCCCGCGCGCGACGTCGCGAA 300
Qy 61 GGGCATCCGGCTTTTACGTCGAAGCGATGCCGACACGCAAGAAAGCTCAAGCTCTTTA 120
Db 301 GGGCATCCGGCTTTTACGTCGAAGCGATGCCGACACGCAAGAAAGCTCAAGCTCTTTA 360
Qy 121 GGTTCGCAAAAGGCTTCAGCCGCGCATCTCCGACGCTACCGCATCAACGACCTCCGC 180
Db 361 GGTTCGCAAAAGGCTTCAGCCGCGCATCTCCGACGCTACCGCATCAACGACCTCCGC 420
Qy 181 TTGCGCGCTCGATTACACGCGCTACAAAACTATAAAGCCCCCATCCACGATTTCAAACTT 240
Db 421 TTGCGCGCTCGATTACACGCGCTACAAAACTATAAAGCCCCCATCCACGATTTCAAACTT 480
Qy 241 TACAGCATCGCGCGTCCGCGATTACGACTTCGACACCCCAATCGCCGTCGCGTCAAAACGAT 300
Db 481 TACAGCATCGCGCGTCCGCGATTACGACTTCGACACCCCAATCGCCGTCGCGTCAAAACGAT 540
Qy 301 CTGCGCGCGCTTGAGCCTCAACCGCGCTTCGCGCTTCGCGCTTCGCGCGCGCGACGCTTC 360
Db 541 TTGCGCGCGCTTGAGCCTCAACCGCGCTTCGCGCTTCGCGCGCGCGACGCTTC 600
Qy 361 AGCAAACTCCATCGGCTCGGCTATGTGACGGCGTAACTATGCGTTACCCGAAT 420
Db 601 AGCAAACTCCATCGGCTCGGCTATGTGACGGCGTAACTATGCGTTACCCGAAT 660
Qy 421 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
Db 661 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 720
Qy 481 GTCGTTCCGCGAACTGTCGCTCGGCTGGCGGTCAAAATCTGA 525
Db 721 GTCGTTCCGCGAACTGTCGCTCGGCTGGCGGTCAAAATCTGA 765
;
RESULT 4
US-08-913-362-29
; Sequence 29, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 810 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria gonorrhoeae
; STRAIN: b2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 241..765
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 241..297

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, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: US 08/406,362
, , FILING DATE: 17-WAR-1995
, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: US 60/001,983
, , FILING DATE: 04-AUG-1995
, , ATTORNEY/AGENT INFORMATION:
, , NAME: Bent, Stephen A.
, , REGISTRATION NUMBER: 29,768
, , REFERENCE/DOCKET NUMBER: 047998/0128
, , TELECOMMUNICATION INFORMATION:
, , TELEPHONE: (202)672-5300
, , TELEFAX: (202)672-5399
, , TELEX: 904136
, , INFORMATION FOR SEQ ID NO: 29:
, , SEQUENCE CHARACTERISTICS:
, , LENGTH: 528 base pairs
, , TYPE: nucleic acid
, , STRANDEDNESS: single
, , TOPOLOGY: linear
, , MOLECULE TYPE: other nucleic acid
, , DESCRIPTION: /desc = "consensus"
US-08-913-362-29

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Query Match      95.5%; Score 501.2; DB 3; Length 528;
Best Local Similarity 95.1%; Pred. NO. 2e-131;
Matches 502; Conservative 22; Mismatches 1; Indels 3
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Qy	1	ATGAAAAAGACATTGCCACACTGATTGCCCTCGCTCTCCGGCGCGCGCACTGGCGAA	60
Db	1	ATGAAAAAGACATTGCGCACATGATTGCCCTCGCHTCTCCGGCGCGCGCACTGGCGAA	60
Qy	61	GGCGCATCTCGGCTTTTAGTCCAAAGCCGATCCGCACACGCAAAAGCCTCAAGTCTTTTA	120
Db	61	GGCGCATCTCGGCTTTTAGTCCAAAGCCGATCCGCACAGCGAAAGCCTCAAGTCTTTTA	120
Qy	121	GGTTCTGCAAAAGCTTCAAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	180
Db	121	GGTTCTGCAAAAGCTTCAAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	180
Qy	181	TTGCGCGTTCGATTACACGCGCTCAAAAACTATA--AAGCCCATCCACCGATTTCAAA	237
Db	181	TTGCGCGTTCGATTACACGCGCTCAAAAACTATAAAGTCCCATCCACCGATTTCAAA	240
Qy	238	CTTTACAGCATCGGCGGTCGCGCATTTACGACTTCGACACCCATATGCGCGTCAAAACG	297
Db	241	CTTTACAGCATCGGCGGTCGCGCATTTACGACTTCGACACCCATATGCGCGTCAAAACG	300
Qy	298	TATCTCGGCGGCGCTTGAGCGCTCAACGCGCGCTCCGTCGACTTGGGCGGACGACAGC	357
Db	301	TATCTCGGCGGCGCTTGAGCGCTCAACGCGCGCTTCCGCTTTCGCTTTCGCGGACGAC	360
Qy	358	TTACGCAAAACCTCCATCGGCGCTCGGCGTATTTGACGCGCGTAAAGCTATGCGGTTACCCCG	417
Db	361	TTACGCAAAACCTCCATCGGCGCTCGGCGTATTTGACGCGCGTAAAGCTATGCGGTTACCCCG	420
Qy	418	AATGTCGATTGGATGCGGCTACGCGTACAACTACATCGGCAAGTCAACACTGTCAAA	477
Db	421	AATGTCGATTGGATGCGGCTACGCGTACAACTACATCTCHGAAAGTCAACACTGTCAAA	480
Qy	478	AACGTCCGTTCCGCGAACTGTGCTCGGCGTGGCGGTCGCGTCAAAATCTGA	525
Db	481	AAATGCGGTTCCGCGAACTGTGCGGCGTGGCGGTCGCGTCAAAATCTGA	528

RESULT 5
US-08-913-362-3
; Sequence 3, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee

APPLICANT: Rioux, Clement
 TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
 TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Iardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/913,362
 FILING DATE: 13-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/406,362
 FILING DATE: 17-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/001,983
 FILING DATE: 04-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Bent, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 047998/0128
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 710 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Neisseria meningitidis
 STRAIN: MCH88
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 116..643
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 116..172
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 173..643
 US-08-913-362-3

Query Match	93.6%	Score 491.2;	DB 3;	Length 710;
Best Local Similarity	97.0%;	Pred. No. 1.5e-128;		
Matches 512;	Conservative	0;	Mismatches 13;	Indels 3;
				Gaps 1;

Qy	1	ATGAAAAAGCACTTGGCACACTGATTCGCCTCGCTCTCCCGCGCGCGCACTGGCGGAA	60
Db	116	ATGAAAAAGCACTTGCGCACTGATTCGCCTCGCCCTCCGCGCGCGCACTGGCGGAA	175
Qy	61	GGCGATCCGGCTTTACGTCCAAGCCGATGGCGCACAGGCAAAAGCCTCAAGCTCTTTA	120
Db	176	GGCGCATCCGGCTTTACGTCCAAGCCGATGGCGCACAGGCAAAAGCCTCAAGCTCTTTA	235
Qy	121	GGTTCGCAAAAGCTTCAGCCCGCGCATCTCCGAGGCTACCGGATCAAGCACCTCCGC	180
Db	236	GGTTCGCAAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGGATCAAGCACCTCCGC	295
Qy	181	TTGCGCGTCGATTACACGCGCTACAAAACTATA---AAGCCCCCTCCACCGATTTCAAA	237

Db 296 TTGCGCGTGGATTACACGGCTACAAAAAATATAAAGTCCCATCCACGGATTTCAAA 355
Qy 238 CTTTACAGCATCGCGCGCTCGCGCATTTACGACTTCGACACCCCAATCGCCCGTCAAAACCG 297
Db 356 CTTTACAGCATCGCGCGCTCGCGCATTTACGACTTCGACACCCCAATCCCGCGTCAAAACCG 415
Qy 298 TATCTCGCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGGGGGGAGGACGACG 357
Db 416 TATCTCGCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTAAACGGGAGGACGACG 475
Qy 358 TTCAGCAAACTCATCGCGCTCGCGCTATTTAGGGGGGTAAGCTATCGCGTTACCCCG 417
Db 476 TTCAGCAAACTCATCGCGCTCGCGCTATTTAGGGGGGTAAGCTATCGCGTTACCCCG 535
Qy 418 AATGTCCGATTTGGATGCGCGGTACCGCTACCACTACATCGGCAAAAGTCAACACTGTCAAA 477
Db 536 AATGTCCGATTTGGATGCGCGGTACCGCTACCACTACATCGGCAAAAGTCAACACTGTCAAA 595
Qy 478 AACGTCCGTTCCGGCGAACTGTCCGTGCGCGGTGCGCGTCAAAATCTGA 525
Db 596 AATGTCCGTTCCGGCGAACTGTCCGTGCGCGGTGCGCGTCAAAATCTGA 643

RESULT 6

US-09-614-912-175
; Sequence 175, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: B01378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 175
; LENGTH: 1919
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-614-912-175

Query Match 9.5%; Score 49.8; DB 4; Length 1919;
Best Local Similarity 49.8%; Pred. No. 0.00035;
Matches 126; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 125 CTGCCAAAGGCTTCAGCGCGCATCTCGGAGGCTACGCGACTCAACGACCTCGCGTTTCG 184
Db 396 CGCGCTACCGCGCTTCCTCCACCATGGCGGACCCCACTGGAGGACAAAGCTACTACGC 455
Qy 185 CCGTCGATTACACGCGCTACAAAAAATATAAAGCCCAATCCACCGATTTCAACTTTACA 244

Db 456 CGTTCGACCTCGAGTCCTCTGCTTCTACTCCGGGCCAAGACCAAGCCCAAGCTCAACA 515
Qy 245 GCATCGCGGGTTCGCCCATTTACGACTTCGACACCCCAATCGCCCGTCAAAACCGTATCTCG 304
Db 516 GCCTCGACGAGGTGACACCCCGAGCTGCTCAAGACCTTCGACCGCTCGGGATCCCTCTCG 575
Qy 305 GCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTGGGGGGGAGGACGACGACTTCAGCC 364
Db 576 GCGAGCAGAGCGCTCTCCAAAGTTCGCGCGCTCGAGCGCGTATCGACTCCACCTCCATCG 635
Qy 365 AAACCTCCATCGG 377
Db 636 CCACCACCCACCG 648

RESULT 7

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 8.7%; Score 45.6; DB 3; Length 4403765;
Best Local Similarity 44.6%; Pred. No. 0.094;
Matches 180; Conservative 0; Mismatches 224; Indels 0; Gaps 0;
Qy 10 GCATTCGCACACTGATTGCTCTCCCGCGCGCGCGCTGCGGAGGAGGCGCATCC 69
Db 3731458 GCCGTTGCGCGCTTGGCGCGCGCGCGCTGCGGCGCGCTGCTGAGCGCGCGCTT 3731517
Qy 70 GGCTTTTACGTTCAAGCGGATGCGGCACACGCAAAAGCTCTTTAGTTCTGCC 129
Db 3731518 GCCCGCGCGCGCGCTTGGCGCGCGCGCGCTTGGCTTCCGGGCGCTCCCGACCGCC 3731577
Qy 130 AAAGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGTTGCGCGTC 189
Db 3731578 GTAGCGCGCGTTGCGCGCGCGCGCGCAAAACCCAGTCTCGGAGACGCGCGCTT 3731637
Qy 190 GATTACACGCGCTACAAAAAATAAAGCCCATCTCCACCGATTTTCAAGCATC 249
Db 3731638 GAGCGCGCGCTTGGCGCTAAGGAATGCGCGCATCCCGCTGCGCGCGCTTACCGCGTT 3731697
Qy 250 GCGCGCTCGCGCATTTTACGATTTCGACACCCCAATCGCCCGCTCAAAACCGTATCTCGCGCG 309
Db 3731698 GCGCGCTGTCGCGCTTCCCGCGCGATGTCGCGCGCTGCGCGCGGAGCGCGCGCGCC 3731757
Qy 310 CGCTTGAGCTCAACCGCGCTCCGTCGACTTGGGGGGGAGGACGACTTCAGCAAAAC 369
Db 3731758 GGCACCGCGCTCCCGCGCGCGCGCGGACACCCCGCAACCGTACGAAAGTCCCGCGC 3731817
Qy 370 TCCATCGCGCTCGCGCTATTGACGGGGTAAAGCTATGCGGTTAC 413
Db 3731818 GCGCGCGGACCGCGCGCGCGCTGGGCGACCCCAACCGCGTGC 3731861

RESULT 8									
US-09-103-840A-1									
; Sequence 1, Application US/09103840A									
; Patent No. 6294328									
; GENERAL INFORMATION:									
; APPLICANT: FLEISCHMAN, Robert D.									
; APPLICANT: WHITE, Owen R.									
; APPLICANT: FRASER, Claire M.									
; APPLICANT: VENTER, John C.									
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM									
; TITLE OF INVENTION: TUBERCULOSIS									
; FILE REFERENCE: 24366-20007.00									
; CURRENT APPLICATION NUMBER: US/09/103,840A									
; CURRENT FILING DATE: 1998-06-24									
; NUMBER OF SEQ ID NOS: 2									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 1									
; LENGTH: 4411529									
; TYPE: DNA									
; ORGANISM: Mycobacterium tuberculosis									
; OTHER INFORMATION: H37Rv									
US-09-103-840A-1									
Query Match 8.7%; Score 45.6; DB 3; Length 4411529;									
Best Local Similarity 44.6%; Pred. No. 0.095;									
Matches 180; Conservative 0; Mismatches 224; Indels 0; Gaps 0;									
QY	10	GCATCTGCCACATGATTGCCCTCGCTCTCCCGCGCGCGCACTGGCGGAAGCGGCATCC	69						
Db	3739165	GCCTTTGCCGCCCTTGCCCGCGCGCGCGCTGCCCGCGCGTGTGTCTGACGCCGCGTT	3739224						
QY	70	GGCTTTTACGTCTCAAGCCGATGCCGACACGCAAAAGCCTCAAGCTCTTTAGTTCCTGCC	129						
Db	3739225	GCGCGCGCGCGCGCTTGCGCGCGAGGCGCGCATTTGCCCTTCGGGCGCTCCCGACCGCC	3739284						
QY	130	AAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTTCGCTTCGCGCTC	189						
Db	3739285	GTAGCCGCTTGCGCGCGCGCGCGCAACACCCAGTCTCGAGACGCGCGCTTGCGCGC	3739344						
QY	190	GATTACAGCGCTACAAAACATAAAGCCCATCCACCGATTTCAAATTTACAGCATC	249						
Db	3739345	GAGCGCGCGCTTGCCGCGCTTAAGAAATGCGCGCACCGCGCTACCGCGCT	3739404						
QY	250	GGCGCGTCCGCCATTTACGATTCGACACCCCAATCGCCGCTCAAACCGTATCTCGCGCG	309						
Db	3739405	GCGCGCTTGCGCGCTTCCCGCGCGATGCGCGCTTGCGCGCGAGCGCGCGACCCCGCC	3739464						
QY	310	CGCTTGAGCCTCAACCGCGCTCCGCTCGACTTGGGCGCGAGCGACAGCTTCAGCCAAACC	369						
Db	3739465	GGCACCGCGCTCCCGCGCGCGCGCACACCGCAACACCGCTAGCAAGATCGCCCGC	3739524						
QY	370	TCCATCGCGCTCGCGGTATTGACGGCGGTAAAGTATGCGCGTTAC	413						
Db	3739525	GCGCGCGGAGACCGCGCGCGCGCTGGGCGCACCAACCCCGGTGC	3739568						

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RESULT 9
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1

```

```

; SEQ ID NO 2
;
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
;
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

```

Query Match	8.6%;	Score 45;	DB 3;	Length 4403765;
Best Local Similarity	44.9%;	Pred. No. 0.14;		
Matches 171;	Conservative 0;	Mismatches 210;	Indels 0;	Gaps 0;
QY	133	GGCTTCAGCCGGGCATCTCGCAGGCTACCGCATCAACGACCTCCGCTTCGCCCGTCGAT	192	
Db	427071	GGCATCGGGGTGACCGCGHAGGGTTGTCCGGCTTCAGTCCCTGCAATCTCGGCGCCGGC	427012	
QY	193	TACACCGCGCTACAAAAAATAAGGCCCAATCCACCGATTTCAAATTTTACAGCATCGCG	252	
Db	427011	AACACCGGTTCTTCAACTCGGCACCGCCAAACACCGGCTTGTTCAACTCCGGCACCGCG	426952	
QY	253	GGCTCGCGCATTTACGACTTCGACACCAATCGCCCGTCAACCGTATCTCGCGCGCGCG	312	
Db	426951	AACACCGGCTTGTTCAACTCGGCACCGGCACGCTCGGCATCTGGCAACATGGGCACCGCG	426892	
QY	313	TTGAGCCTCAACCGCGCGCTCCGTCCGACTTTGGCGCGCAGCAGCTTCAGCGCAACCTCC	372	
Db	426891	GGCTTCGGCGTCGCGCTATCCGGCGACAGCCAGGTGGGCATCTGGCGCACCACTCGCGC	426832	
QY	373	ATCGGCTTCGGCGTATTGACGGGCGTAACTATCGCTTACCCGGAATGTGCAATTTGAT	432	
Db	426831	AGTTTCAACATCGGCTTGTTTAACTCGGCACCGGCATGTCCGCATCTCGCAACTCGCGC	426772	
QY	433	GCGCGCTACCGCTACAACTACATCGGCAGAAAGTCAACACTGCAAAAAAGTCCGTTCCCGC	492	
Db	426771	ACCGGCNAAGTTCGGCATCGGCAACACCGGCACCGGCACACCGGCATCTCGAAACAGCGCG	426712	
QY	493	GAAGTGTCCGTCGGCGTGGCG	513	
Db	426711	AACTTCAACACCGGCTTGTCTC	426691	

```

RESULT 10
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

```

Query Match 8.6%; Score 45; DB 3; Length 4411539;
Best Local Similarity 44.9%; Pred. No. 0.14;
Matches 171; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

QY 133 GGCTTCAGCCGGCGCATCTCGCAGGTCACGCATCAACGACCTCCGCTTCGCCGTCGAT 192

Db 426913 GGATCTGGGTGTACCGCGCAGCGGTTGTCGGGTTTCAGCTCCCTGAATCGCGGCCCGC 426954

Qy 193 TACAGCGCTACAAAACTATAAGCGCCATCCACCGATTTCAAATTTTACAGCATCGGC 252
 Db 426853 AACACCGGTTTCTTCAACTCGCGCACCGCCACACACCGGCTTGTTCAACTCGGCGACCGGC 426794
 Qy 253 GCGTCCGCGCTTTACGACTTCGACACCAATCGCCCGTCAACCGTATCTCGGCGCGGC 312
 Db 426793 AACACCGGCTTGTTCAACTCGGCGCACCGGCAACGTCGCGATCGGCAACATCGGCGC 426734
 Qy 313 TTGAGCCTCAACCGCGCTCCGTCGACTTGGCGCGCGACGAGCTTCAGCAAAACCTCC 372
 Db 426733 GGCTTCGGCGTCGCGCTATCGGCGACAGCCAGTGGGATCGGCGACCACTCGGC 426674
 Qy 373 ATCGGCTCGCGCTATTGACGGGCGTAAAGTATGCGGTATCCCGAATGTCGATTTGGAT 432
 Db 426673 AGTTTCAACATCGGCTTGTTCAACTCGGCGCACCGGCAATGTCGCGATCGGCAACTCGGC 426614
 Qy 433 GCGGCTACCGCTACAACTACATCGGCAAGTCAACCTGTAACAAAGCTCGTTCGCGC 492
 Db 426613 ACCGCAACGTGCGCATCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCA 426554
 Qy 493 GAACTGTCCGTCGCGGTCGCGC 513
 Db 426553 AACTACAACCGGCTTGTCTC 426533

RESULT 11
 US-09-881-165-4
 ; Sequence 4, Application US/09881165
 ; Patent No. 6632930
 ; GENERAL INFORMATION:
 ; APPLICANT: HOOD, ELIZABETH
 ; APPLICANT: HOWARD, JOHN
 ; APPLICANT: BAYLEY, MICHELE
 ; APPLICANT: GASTEL, FRANS VAN
 ; APPLICANT: WANG, HUAMING
 ; APPLICANT: WARD, MICHAEL
 ; APPLICANT: WOODARD, SUSAN
 ; TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
 ; TITLE OF INVENTION: ENZYMES PRODUCED IN PLANTS
 ; FILE REFERENCE: 10032R
 ; CURRENT APPLICATION NUMBER: US/09/881,165
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: 60/211,732
 ; PRIOR FILING DATE: 2000-06-15
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 1082
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding
 ; OTHER INFORMATION: Organophosphate Hydrolase
 US-09-881-165-4

Query Match 8.4%; Score 44; DB 4; Length 1082;
 Best Local Similarity 46.0%; Pred. No. 0.012;
 Matches 149; Conservative 0; Mismatches 175; Indels 0; Gaps 0;
 Qy 31 CTCGCTCTCCGCGCGCGCTACCTGCGGAGCGCATCCGCTTTTACGTCCAGCGCAT 90
 Db 522 CTCGTGCTCAAGGCGCGCGCGCGCTCCCTCGGCAACCGGCTCGGTCGCGGTCACCA 581
 Qy 91 GCGGCAACGAAAGCTCTTCTTCTGTTCTGCAAGGCTTCAGCGCGCGCATC 150
 Db 582 ACCGCGGCTCCACGCGGAGCGGAGGAGCGGCGGCGCATCTTCAGTCCGAGGCGCTC 641
 Qy 151 TCCGAGGCTACCGCATCAACGACCTCGCTTCGCGCTGATTACACGCGGTACAAAAC 210
 Db 642 TCCCGTCCGCGGTGTGATCGGCGACCTCCGACGACGAGGACCTCTCTTACCTACC 701
 Qy 211 TATAAGCGCCCATCCCGATTTCAAACTTTTACAGCATCGGCGCGTCCGCCATTTACGAC 270

Db 702 GCCTCGCGCGCGCGCTACCTATCGGCTCGACACATCCGCACTCGGCATCGGC 761
 Qy 271 TTGACACCACTCGCGCTCAAAACCGTATCTCGGCGCGCGCTTGAGCTTCAACCGCGCC 330
 Db 762 CTCGAGGACAAAGCTTCGCGCTCGGCTCTCTCGGATCGCTCTCTGGCAGACCGCGCC 821
 Qy 331 TCGTTCGACTTGGCGCGCGGAC 354
 Db 822 CTCCTCATCAAGCGCTCATCGAC 845

RESULT 12
 US-08-961-527-363
 ; Sequence 363, Application US/08961527
 ; Patent No. 6420135
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 391
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/961,527
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PB340P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 363:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4483 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 US-08-961-527-363

Query Match 8.4%; Score 44; DB 3; Length 4483;
 Best Local Similarity 47.3%; Pred. No. 0.021;
 Matches 174; Conservative 0; Mismatches 185; Indels 9; Gaps 1;
 Qy 134 GCTTCAGCGCGCGCATCTCGGAGGCTACGCGCATCAACGACCTCGGCTTCGCGCTCGATT 193
 Db 2659 GCTTCAGCAAGTACGAGTGGCTCGGCTTCAGCATCAACGAGTGTTCAGTCTCAGCTCA 2718
 Qy 194 ACAGCGCTACAAACCTATAAGCCCGCATCCACCGATTTCAAACTTTTACAGCATCGCGC 253
 Db 2719 ACCAGTGCCTCTGAATCAGCATCAACGAGTGCCTCGGCTTCAGCAAGCAGCAGTGGTGC 2778
 Qy 254 GGTCCGCGATTTA-----CGACTTCGACACCGAATCCCGCTTCAACCGTATCTCG 304
 Db 2779 GCTTCAGCAAGTACTAGTGTGATCGGCTTCAGCATCGACAGTGGTCTTGAATCGGCATCA 2838
 Qy 305 GCGCGCGCTTACGCTCAACCGCGCTTCGTCGACTTGGGCGGCGAGCAGCTTCAGCC 364
 Db 2839 ACAGTGTCTCGGCTTCAGCATCAACGAGTGCCTCAGCTCAGCAAGCAGCATAGCTTCT 2898

QY 365 AAACCTCCATCGGCTTCGGCGTATTGACGGGGTAAAGTATGCGTTACCCGGAATGTG 424
 Db 2899 GAATGTGATCAACAGTGGTCCGCTTCAGCGTCAACAGTGGTTCAGCGTTCG 2958
 QY 425 ATTGATGCGGCTACCGCTCAACTACATCGGCAAGTCAACACTGTCAAAAAGTCC 484
 Db 2959 ACAAGTGTCTCGGCTTCAGCATCAACAGTGGTTCGGCTTCAGCAAGCGCAAGTACCTCA 3018
 QY 485 GTTCGGGC 492
 Db 3019 GGTTCAGC 3026

RESULT 13
 US-08-961-527-71
 ; Sequence 71, Application US/08961527
 ; Patent No. 6420135
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 391
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/961,527
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PB340P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 71:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 32768 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 US-08-961-527-71

Query Match 8.4%; Score 44; DB 3; Length 32768;
 Best Local Similarity 47.3%; Pred. No. 0.043;
 Matches 174; Conservative 0; Mismatches 185; Indels 9; Gaps 1;
 QY 134 GCTTACCGCGGCTTCGGGAGGTACCGGATCAACGACCTCCGCTTCGGCGTGGATT 193
 Db 1442 GCTTACGAAAGTACCAAGTGGTTCAGCATCAACGAGTCTTCAGTCTCAGCGTCA 1501
 QY 194 ACACGGCTTACAAAATATAAGCCCCATCAACGATTTCAAACCTTTACAGCATCGGG 253
 Db 1502 ACCAGTGCCTCTGAATCAGATCAACAAAGTGCTTCGGCTTCAGCAAGCAACAGTGGTGG 1561
 QY 254 GCTCCGCCATTTA-----CGACTTCGACACCCCAATCGCCCGTCAAAACCGTATCTCG 304
 Db 1562 GCTTACGAAAGTACTAGTGCATCGGCTTCAGCATCGAAGTGGTCTGAAATCGGGCATCA 1621
 QY 305 GCGCGGCTTGAGCCTCAACCGGCGCTTCGCTCGACTTGGGGCGCAGCAGCTTCAGCC 364

Db 1622 ACAGTGTCTTCGGCTTCAGCATCAACAGTGGTTCAGCTCAGCAAGCATCAGCTTCT 1681
 QY 365 AAACCTCCATCGGCTTCGGCGTATTGACGGGGTAAAGTATGCGTTACCCGGAATGTG 424
 Db 1682 GAATGTGATCAACAGTGGTCCGCTTCAGCGTCAACAGTGGTTCAGCGTTCG 1741
 QY 425 ATTGATGCGGCTACCGCTCAACTACATCGGCAAGTCAACACTGTCAAAAAGTCC 484
 Db 1742 ACAAGTGTCTCGGCTTCAGCATCAACAGTGGTTCGGCTTCAGCAAGCGCAAGTACCTCA 1801
 QY 485 GTTCGGGC 492
 Db 1802 GGTTCAGC 1809

RESULT 14
 US-09-197-649-7
 ; Sequence 7, Application US/09197649
 ; Patent No. 6194550
 ; GENERAL INFORMATION:
 ; APPLICANT: Gold, Larry
 ; APPLICANT: Tuerk, Craig
 ; APPLICANT: Pribrnow, David
 ; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
 ; FILE REFERENCE: NEX02/C1-CON
 ; CURRENT APPLICATION NUMBER: US/09/197,649
 ; CURRENT FILING DATE: 1998-11-23
 ; EARLIER APPLICATION NUMBER: 07/829,461
 ; EARLIER FILING DATE: 1992-01-31
 ; EARLIER APPLICATION NUMBER: 07/739,055
 ; EARLIER FILING DATE: 1991-08-01
 ; EARLIER APPLICATION NUMBER: 07/561,968
 ; EARLIER FILING DATE: 1990-08-02
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 390
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Sequence
 ; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
 ; OTHER INFORMATION: fragments having NcoI restriction sites.
 US-09-197-649-7

Query Match 8.3%; Score 43.6; DB 3; Length 390;
 Best Local Similarity 45.0%; Pred. No. 0.011;
 Matches 163; Conservative 0; Mismatches 199; Indels 0; Gaps 0;
 QY 147 CATCTCCGAGGCTACCGCATCAACGAGCTTCGGCTTCGGCGTATTACACGCGTACAA 206
 Db 5 CATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 64
 QY 207 AAACCTATAAGCCCATCCACGATTTCAAACCTTTACAGCATTCGGCGGCTTCGCGCATTTA 266
 Db 65 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 124
 QY 267 CGACTTCGACACCCCAATCGCCGTCACACCGTATCTCGCGCGCGCTTCGAGCTCAACCG 326
 Db 125 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 184
 QY 327 CGCCTTCGCTTCGACTTGGGCGGCGACGAGCTTCAGCCAAACCTTCATCGGCGCTTCGGCGT 386
 Db 185 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 244
 QY 387 ATTGACGGCGTAACTATGCGTTACCCGGAATGTGATTTGGATTCGGGCTACGGCTA 446
 Db 245 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 304
 QY 447 CAACTACATCGGCAAGTCAACACTGTCAAAACCTTCGTTCCGGCGGAACCTGTCGTCGG 506

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 13:08:07 ; Search time 7695 Seconds
(without alignments)
2596.977 Million cell updates/sec

Title: US-10-650-123-1

Perfect score: 525
Sequence: 1 atgaaaaagcacttgcac.....gcgtgcgcgtcaaatctga 525

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gss1.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57.8	11.0	622	6	CA197724 SCAGAD107
2	56.4	10.7	626	6	CA193415 SCCCFLL100
3	55.2	10.5	787	6	CB654660 OSJNEC07F
4	53.6	10.2	591	6	CB640993 OSJNEA17F
5	53.6	10.2	665	7	CV152413 LS245-S-S
6	53.6	10.2	698	6	CB653730 OSJNEC05A
7	53.6	10.2	725	6	CB677411 OSJNEE14E
8	53.6	10.2	741	7	CF589226 EST00F06
9	53.6	10.2	759	6	CB671800 OSJNEE05I
10	53.6	10.2	762	6	CB677339 OSJNEE14C
11	53.6	10.2	775	6	CB677062 OSJNEE13K
12	53.6	10.2	778	6	CB654692 OSJNEC07G
13	53.6	10.2	782	6	CB665147 OSJNEE11F
14	53.6	10.2	842	6	CB6668023 OSJNEE15K
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16	53.4	10.2	644	7	CF315326 HD--04-D0
17	52.2	9.9	525	7	CF308604 ABF--02-H
18	52	9.9	696	6	CF308604 OV.101M15
19	51.8	9.9	530	7	CF335206 JMT--04-M
20	51.8	9.9	558	4	BG560231 RH122 71
21	51.8	9.9	655	6	CA172233 SCSPB107
22	51.8	9.9	693	6	CA253038 SCJPL409
23	51.8	9.9	773	6	CA231223 SCQSFL303
24	51.2	9.8	519	7	CV097296 FAMU_USDA

25	50.8	9.7	691	8	BH898151	BH898151	MB61p2A7
26	50.6	9.6	649	6	CD219573	CCC1_57_A	
27	50.6	9.6	666	6	CD222538	CCC1_22_G	
28	50.6	9.6	669	6	CD222866	CCC1_24_B	
29	50.2	9.6	744	6	CB681064	OSJNEf06N	
30	50.2	9.6	1170	9	CL978445	OsIFCC031	
31	50.2	9.6	2397	9	CL973983	OsIFCC025	
32	50	9.5	670	4	BJ748832	BJ748832	
33	49.8	9.5	2667	9	CL971648	CL971648	OsIFCC021
34	49.2	9.4	881	6	CB643751	OSJNEB04J	
35	49.2	9.4	1196	7	CK167632	FGAS05203	
36	49	9.3	515	4	BG560157	RH122 71	
37	49	9.3	645	1	AI389106	GH20152_5	
38	49	9.3	662	6	CD223038	CCC1_25_B	
39	48.8	9.3	559	2	AW680997	WSL_9_E10	
40	48.8	9.3	567	2	BE593027	WSL_93_D1	
41	48.8	9.3	620	2	BE357605	DG1_21_E0	
42	48.8	9.3	658	6	CD463595	ETHI_45_F	
C 43	48.8	9.3	954	7	CO250025	AGENCOURT	
C 44	48.8	9.3	1176	9	CL974133	OsIFCC042	
C 45	48.6	9.3	485	6	CD888257	GL18_1071	

ALIGNMENTS

RESULT 1
CA197724
LOCUS SCAGAD1074C04.g AD1 Saccharum officinarum cDNA clone SCAGAD1074C04
DEFINITION 5', mRNA sequence.
ACCESSION CA197724
VERSION CA197724.1 GI:35228269
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 622)
Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: paruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 074 row: C column: 04
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..622
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/lab host="SCAGAD1074C04"
/clone lib="DH10B"
/note="Organ: seedlings inoculated with Gluconacetobacter
diaetrophicans; Vector: pSporti; Site_1: Salt; Site_2:
Not; An unidirectional cDNA library generated from
[seedlings inoculated with Gluconacetobacter
diaetrophicans]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-column and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details

FEATURES
source
1..622
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/lab host="SCAGAD1074C04"
/clone lib="DH10B"
/note="Organ: seedlings inoculated with Gluconacetobacter
diaetrophicans; Vector: pSporti; Site_1: Salt; Site_2:
Not; An unidirectional cDNA library generated from
[seedlings inoculated with Gluconacetobacter
diaetrophicans]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-column and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details

of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>

```

ORIGIN
Query Match      11.0%; Score 57.8; DB 6; Length 622;
Best Local Similarity 47.4%; Pred. No. 4.3e-05;
Matches 173; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 27 TGCCCTCGCTCTCCCGCGCCGCGCACTGGCGGAAGCGCATCCGGCTTTTACGTCCAAGC 86
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 108 TGATCGCTCTCTCGCGATCGCATCAATCACCGCGCGGAGTCCCGGTGACGCCGACG 167
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QY 87 CGATGCGGCACACGAAAGCCTCAAGCTCTTTAGTTTCGCAAAAGGCTTCAGCCCGCG 146
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Db 168 CGCCACCGTCAAACTCCCGCGCCGCGCGCCCGCGCTCAGGCGCTCCAGCAGGCA 227
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QY 147 CATCTCGGAGGTACCGCATCAACGCTTCGCGCTTCGCGCTGATTACAGCGCTACAA 206
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Db 228 ACCGCTCTCCCGCGCCACCGCACCTCTCCCGCGCTCCGAGCAGCACGCGCCCGCG 287
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QY 207 AAATATAAGCCCGCATCCACCGATTTCAAACTTTACAGCATCGCGCGCTCCGCCATT 266
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Db 288 CACCACCGACACGCTTCTCCGGTCCCAACAGCGGTCCCGCGCCCGCGACCACTC 347
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QY 267 CGACTTCGACACCAATCGCCGCTCAACCGTATCTCGCGCGCGCTTTAGCGCTCAAC 326
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Db 348 CTTCTCAGCGCCACACAGCGCTCTCCGTCACCGTCGCGAGCGCGCTACCGGTCCCA 407
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QY 327 CGCCTCGCTGACTTGGCGGACGACAGCTTCAGCCAACTCATCGGCTTCGGCT 386
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Db 408 CCACTCCGTCGACTTCCCGCGGTGAGCCGACACCGGTCCCGGACCCCTTCGCCGT 467
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QY 387 ATTGA 391
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Db 468 CTTCA 472
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RESULT 2
CA193415      626 bp mRNA linear EST 24-SEP-2003
LOCUS        SCCCL1003E05.g FL1 Saccharum officinarum cDNA clone SCCCL1003E05
DEFINITION   5', mRNA sequence.
ACCESSION    CA193415
VERSION      CA193415.1 GI:35140555
KEYWORDS     EST.
SOURCE       Saccharum officinarum
ORGANISM     Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE    1 (bases 1 to 626)
AUTHORS      Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE        The libraries that made SUCEST
JOURNAL      Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT      Contact: Arruda P
              Centro de Biologia Molecular e Engenharia Genetica
              Universidade Estadual de Campinas
              Caixa Postal 6010, 13083-970, Campinas SP, Brazil
              Tel: 55 19 3788 1137
              Fax: 55 19 3788 1089
              Email: parruda@unicamp.br
              Clone distribution: clone distribution information can be found
              through the Brazilian Clone Collection Center (BCCC) at
              http://www.bcccenter.fcav.unesp.br
              Plate: 003 row: E column: 05
              Seq primer: T7 Promoter Primer.
              Location/Qualifiers
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                  /mol_type="mRNA"
                  /db_xref="taxon:4547"
                  /clone="SCCCL1003E05"

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source

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/lab_host="DH10B"
/clone_lib="FL1"
/note="Organ: Inflorescence at beginning of development
(1cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
An unidirectional cDNA library generated from
[Inflorescence at beginning of development (1cm-long)].
cDNA was prepared from polyA+ mRNA using SuperScript
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 Kb were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucet.lad.ic.unicamp.br/public"

ORIGIN
Query Match      10.7%; Score 56.4; DB 6; Length 626;
Best Local Similarity 47.2%; Pred. No. 0.00011;
Matches 171; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

QY 27 TGCCCTCGCTCTCCCGCGCCGCACTGGCGGAAGCGCATCCGGCTTTTACGTCCAAGC 86
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Db 58 TGATCGCTCTCTCGCGAGCGCAGTCAACCGCGGCGAGCCCGCGCGCGGACCGAACC 117
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QY 87 CGATGCGGCACACGAAAGCCTCAAGCTCTTTAGTTTCGCAAAAGGCTTCAGCCCGCG 146
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Db 118 CGCCACCGTCAAACTCCCGCGCCGCGCGCCCGCGCTCAGGCGCTCCGCGCAGGCA 177
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QY 147 CATCTCCGAGCTACCGCATCAACGCTTCGCGCTTCGCGCTGATTACAGCGCTACAA 206
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Db 178 ACCGCTTACCGCGCCACCGCACCTCTCCCGCGCTCCGAGCAGCACCGCGCCCGCG 237
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 207 AAATATAAGCCCGCATCCACCGATTTCAAACTTTACAGCATCGCGCGCTCCGCCATT 266
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Db 238 CACCACCGACACGCTCTCTCCGGTCCCAACAGCGCGCCCGCGCGCGGACCACTC 297
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QY 267 CGACTTCGACACCAATCGCCGCTCAACCGTATCTCGCGCGCGCTTTAGCGCTCAAC 326
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QY 327 CGCCTCCGTCGACTTGGCGGCGAGCAGCATCTTCAGCCAACTCATCGGCTTCGGCGT 386
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Db 358 CCACCTCCGCGCGGTCTCCCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGT 417
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QY 387 AT 388
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Db 418 CT 419
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RESULT 3
CA193415      787 bp mRNA linear EST 09-APR-2003
LOCUS        OSJNEC07F21.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
DEFINITION   clone OSJNEC07F21 5', mRNA sequence.
ACCESSION    CB654660
VERSION      CB654660.1 GI:29658385
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 787)
AUTHORS      Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
              Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE        Large-scale identification of ESTs involved in the interaction
              between rice and Magnaporthe grisea
JOURNAL      Unpublished (2003)
COMMENT      Contact: Rod Wing
              Arizona Genomics Institute
              University of Arizona
              Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
              85721-0088, USA
              Tel: 520 626 3967

```

Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: F column: 21
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEal7F21"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match 10.5%; Score 55.2; DB 6; Length 787;
Best Local Similarity 44.7%; Pred. No. 0.00023; Mismatches 263; Indels 0; Gaps 0;
Matches 213; Conservative 0; Mismatches 263; Indels 0; Gaps 0;
QY 41 CGCGCGCGCACTCGCGGAAGCGCATCGCGCTTTTACGTCCAAAGCGCATCGCGCACACG 100
DB 60 CAGCAGCGCCATGAGGATAGGACCGGAGTTCTACCGTTTACCGACGAGCTGCGCG 119
QY 101 CAAAGCCTCAAGCTCTTTAGTTTCGCGAAAGGTTTCAGCCCGCGCATCTCCGAGGCT 160
DB 120 TGCAGACGCGAGCTTCTCCGCGCTCTCCCTCGCGAGTCCATCTGCTCTCCCGCTCG 179
QY 161 ACCGATCAAGACCTCGCTTCGCGTCGATTACACGCGTACAAAACCTATAAGCCC 220
DB 180 ACCGCGCAAGAGCGCGCTTCGACGCGAGTACCAACCTTCTCTCCCGCTCCCGCG 239
QY 221 CATCCACCGATTCAAACTTTACAGCATCGCGCGCTTCGCGCATTTACGACTTCGACACCC 280
DB 240 CAAAGACGCCATCGCCAAACATCAAGCGGTGCGCGGAACCTTGATGCGCGGCTCA 299
QY 281 AATCGCGCTCAACCGTATCTCGCGCGCGCTTCGAGCTCAACCGCGCTTCGCTGCACT 340
DB 300 TCGGCTCGCGCAAGCTCGCTTCGCGCGCACCAAGCGCGAGCGCTTACCAACGCGTCAACC 359
QY 341 TGGCGCGAGCAGCTTCAGCAAACTTCATCGCGCTCGCGCTATTGACGGCGTAA 400
DB 360 TCCCGCTCGACAAACAAACAAACAAAGTCTACGCGCGCGCGCGCGCAAGATCAACAACA 419
QY 401 GTATGCGGTTACCCCGAATGTCGATTTGGATGCGCGGTACCGCTACCACTACATCGGCA 460
DB 420 ACAAGTCAACGCTTCGGTTTCAACAGATGGGGGTTTACAAACAGCAGCAACGCGG 479
QY 461 AAGTCAACACTGTCAAAACGTCGTTCCGCGGAACCTGTCGCTCGCGCTCGCGCTC 516
DB 480 GCGGCAACTACGCGCGCAACGCGCGGAGCTGAAGAGCTACTTCAACAAGTGGTGC 535

RESULT 4
CB640993
LOCUS
DEFINITION OSJNEal7F21.f OSJNEa Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEal7F21 5', mRNA sequence.
CB640993
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 591)

AUTHORS
Jantaauriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: atc agc ggc cgc gat cc
BACKWARD: aat taa ccc tca cta aag gg
Plate: 17 row: F column: 21
Seq primer: atc agc ggc cgc gat cc.
Location/Qualifiers
1..591
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEal7F21"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEa"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; 6 hrs after inoculation with Rice Blast (Che 86061)"

ORIGIN
Query Match 10.2%; Score 53.6; DB 6; Length 591;
Best Local Similarity 44.5%; Pred. No. 0.00063; Mismatches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
QY 41 CGCGCGCGCACTCGCGGAAGCGCATCGCGCTTTTACGTCCAAAGCGCATCGCGCACACG 100
DB 36 CAGCAGCGCCATGAGGATAGGACCGGAGTTCTACCGTTTACCGACGAGCTGCGCG 95
QY 101 CAAAGCCTCAAGCTCTTTAGTTTCGCGAAAGGTTTCAGCCCGCGCATCTCCGAGGCT 160
DB 96 TGCAGACGCGAGCTTCTCCGCGCTCTCCCTCGCGAGTCCATCTGCTCTCCCGCTCG 155
QY 161 ACCGATCAAGACCTCGCTTCGCGTCGATTACACGCGTACAAAACCTATAAGCCC 220
DB 156 ACCGCGCAAGCGCGCGCTTCGACGCGGAGTACCACTTCTCTCCCGCTCCCGCG 215
QY 221 CATCCACCGATTCAAACTTTACAGCATCGCGCGGTTCGCGCATTTACGACTTCGACACCC 280
DB 216 CAAAGACGCCATCGCCAAACATCAAGCGGTGCGCGGAACCTTGATGCGCGGCTCA 275
QY 281 AATCGCGCTCAACCGTATCTCGCGCGCGCTTCGAGCTCAACCGCGCTTCGCTGCACT 340
DB 276 TCGGCTCGCGCAAGCTCGCTTCGCGCGCACCAAGCGCGAGCGCTTACCAACGCGTCAACC 335
QY 341 TGGCGCGAGCAGCTTCAGCAAACTTCATCGCGCTCGCGCTATTGACGGCGTAA 400
DB 336 TCCCGCTCGAACAACAACAACAACAAGTCTTACGCGCGCGCGCGCAAGATCAACAACA 395
QY 401 GCTATGCGGTTACCCCGAATGTCGATTTGGATGCGCGGTACCGCTACCACTACATCGGCA 460
DB 396 ACAAGTCAACGCTTCGGTTTCAACAGATGGGGGTTTACAAACAGCAGCAACGCGG 455
QY 461 AAGTCAACACTGTCAAAACGTCGTTCCGCGGAACCTGTCGCTCGCGCTCGCGCTC 516
DB 456 GCGGCAACTACGCGCGCAACGCGCGGAGCTGAAGAGCTACTTCAACAAGTGGTGC 511

RESULT 5
CV152413

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LOCUS          CV152413                665 bp    mRNA    linear    EST 08-SEP-2004
DEFINITION     LS245-S-SEQ Cold stressed rice cDNA library Oryza sativa (japonica
culturivar-group) cDNA, mRNA sequence.
ACCESSION      CV152413
VERSION        CV152413.1 GI:51946072
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 665)
AUTHORS        Lee, J.-S.
TITLE          Isolation and chromosomal mapping of the rice clones differentially
               induced under abiotic stress conditions
JOURNAL        Unpublished (2004)
COMMENT        Contact: Lee Jung-Sook
               Bioinformatics Team
               National Institute of Agricultural Biotechnology, Rural Development
               Administration
               225 Seodundon, Suwon, 441-707, Korea
               Tel: 82 31 299 1663
               Fax: 82 31 299 1722
               Email: jungles@da.go.kr.
FEATURES-
source         1..665
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="ilpumbyeo"
               /db_xref="taxon:39947"
               /tissue_type="leaf"
               /dev_stage="one week old"
               /clone_lib="Cold stressed rice cDNA library"
               /notes="Vector: pBluescript SK+; Cold treatment by placing
               at 40C for 16 hour after growth on MS medium for one week"

ORIGIN
Query Match    10.2%; Score 53.6; DB 7; Length 665;
Best Local Similarity 44.5%; Pred. No. 0.00063;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 41 CGCGCCGCGACTGGCGGAGGCGCATCGGCTTTAGCTCCAGCGGATCGCGCACAG 100
DB 46 CAGCAGCGGCATGGAGGGATACGACCGCGAGTTCTACCAGTTTCAGCGACAGCTCGCGC 105
QY 101 CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAGGCTTCAGCCGCGCATCTCGCGAGGCT 160
DB 106 TGCAGAGCGGAGCTTCTCGGCTCTCTCTCGGCGACTCCATCTGCTCTCCCTCCG 165
QY 161 ACCGATCAACGACTTCGCTTCGCGTTCGATTCAGCGGCTACAAAACTATAAAGCCC 220
DB 166 ACCGCGCAACGAGCGCGCTTCGAGCGGAGTACCAACCACTTCTCTCCCTCCCGC 225
QY 221 CATCCACCGATTTCAAACTTACAGATCGGCGGCTTGAGCCTCAACCGCGCTCGCTCGACT 280
DB 226 CCAAGAACGCGCATCGGCAACATCAACGGCGTTCGCGGAAACCTGGATGGCGCGGCTCA 285
QY 281 AATCGCCGCTCAAAACCGATATCTCGGCGCGGCTTGAGCCTCAACCGCGCTCGCTCGACT 340
DB 286 TCGGCTCGGCAAGCTCGCTTCGCGGCGCACCAAGCGCGACCGCTACACAGGCTCAAC 345
QY 341 TGGGCGGCGAGCAGCTTTCAGCCAACTTCATCGGCTTCGCGGCTATTTGACGGGGCTAA 400
DB 346 TCCCGCTCGCAACAACAACAACAAGTCTTACGCGGCGCGCGCAAGATCAACAACA 405
QY 401 GCTATCGCGTTACCCGAATGTCGATTTGGATCCCGGCTACCGCTACACTACATCGCA 460
DB 406 ACAACGTCAACGCTTCGCGGTTCAACAAGATGGGGGTTACAAACAGCAGACGACGCG 465
QY 461 AAGTCAACACTGTCAAAAACGTCGTTTCGCGGAACTGTCCGTCGCGGTCGCGCTC 516
DB 466 GCGGCAACTACGCGGCAACGCGGCGGACGCTGAGAGCTACTTCAACAAGTCGCTC 521

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RESULT 6
LOCUS   CB653730
DEFINITION     OSJNEC05A17.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEC05A17 5', mRNA sequence.
ACCESSION      CB653730
VERSION        CB653730.1 GI:29657455
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 698)
AUTHORS        Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
               Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
TITLE          Large-scale identification of ESTs involved in the interaction
               between rice and Magnaporthe grisea
JOURNAL        Unpublished (2003)
COMMENT        Contact: Rod Wing
               Arizona Genomics Institute
               University of Arizona
               Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
               85721-0088, USA
               Tel: 520 626 3967
               Fax: 520 621 9288
               Email: http://genome.arizona.edu
               PCR Primers
               FORWARD: gta aaa cga cgg cca gtg
               BACKWARD: gga aac agc tat gac cat g
               Plate: 05 row: A column: 17
               Seq primer: gta aaa cga cgg cca gtg.
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               /dev_stage="3 week"
               /lab_host="DH10B"
               /clone_lib="OSJNEC"
               /notes="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
               XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match    10.2%; Score 53.6; DB 6; Length 698;
Best Local Similarity 44.5%; Pred. No. 0.00064;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 41 CGCGCGCGCATCGGCGGAGGCGCATCGGCTTTAGCTCCAGCGGATCGCGCACAG 100
DB 47 CAGCAGCGGCGGATGGAGGATACGACCGCGAGTTCTACCAGTCCCGCGACAGCTCGGCG 106
QY 101 CAAAAGCTCTCAAGCTCTTTAGGTTCTGCCAAGGCTTCAGCCCGCGCATCTCGCGAGGCT 160
DB 107 TGCAGAGCGGAGCTTCTCGGCTCTCTCTCGGCGACTCCATCTGCTCTCCCTCCG 166
QY 161 ACCGATCAACGACTTCGCTTCGCGTTCGATTCAGCGGCTACAAAACTATAAAGCCC 220
DB 167 ACCGCGCAACGAGCGCGCTTCGACGGCGAGTACCAACCACTTCTCTCCCTCCCGC 226
QY 221 CATCCACCGATTTCAAACTTACAGATCGGCGGCTTCGCGCATTTACGACTTCGACACC 280
DB 227 CCAAGAACGCGCATCGGCAACATCAACGGCTCGCGGAAACCTGGATGGCGCGGCTCA 286
QY 281 AATCGCCGCTCAAAACCGATATCTCGGCGCGGCTTGAGCCTCAACCGCGCTTCGCTCGACT 340
DB 287 TCGGCTCGGCAAGCTTCGCGGTTCAACAAGATGGGGGTTACAAACAGCAGGCTCAAC 346
QY 341 TGGGCGGCGAGCAGCTTCAGCCAAACCTTCATCGGCTTCGCGGCTATTTGACGGGGCTAA 400

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Db      347 TCCCGTGCACAAACAAACAAAGTCTTACGGCGCGCGCCGAAGATCAACACA 406
Qy      401 GCTATGCGGTTACCCCGAATGTGCAATTTGGATGCGCGCTACCGCTTACAACTACATCGGCA 460
Db      407 ACAAGCTCAACGCCCTTCGGGTTCAACAAGATGGGGGTTACACAACAGCAGCAACGGCG 466
Qy      461 AAGTCAACACTGTCAAAACGTCGTTCCGGGGAACACTGTCGTCGGCGTGGCGGTC 516
Db      467 GCGGCAACTACGGGCGCAACGGCGCGACGCTGAAGAGCTACTTCAACAAGTCGGTC 522

RESULT 7
LOCUS   CB677411 725 bp mRNA linear EST 09-APR-2003
DEFINITION OSJNE14E24.f OSJNE Oryza sativa (japonica cultivar-group) cDNA clone OSJNE14E24 5', mRNA sequence.
ACCESSION CB677411
VERSION   CB677411.1 GI:29681136
SOURCE   EST.
ORGANISM Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 725)
AUTHORS   Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
           Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE     Large-scale identification of ESTs involved in the interaction
           between rice and Magnaporthe grisea
JOURNAL   Unpublished (2003)
COMMENT   Contact: Rod Wing
           Arizona Genomics Institute
           University of Arizona
           Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
           85721-0088, USA
           Tel: 520 626 3967
           Fax: 520 621 9288
           Email: http://genome.arizona.edu
PCR PRIMERS
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: E column: 24
Seq primer: gta aaa cga cgg cca gtc.
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     /tissue_type="Leaf"
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     /lab_host="DH10B"
     /clone_lib="OSJNE"
     /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
           XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

Query Match      10.2%; Score 53.6; DB 6; Length 725;
Best Local Similarity 44.5%; Pred. No. 0.00064;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy      41 CGCGCGCGCACTGCGGGAAGCGCATCCGGCTTTTACGTCCAAAGCGGCGGCGCACAG 100
Db      22 CAGCAGCGCCATGGAGGATACGACCGGAGTTCTACAGTTACGACACAGCTGCGGC 81
Qy      101 CAAAAGCCTCAAGCTCTTTAGTCTTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCT 160
Db      82 TGCAGACGGGAGCTTCTCCGCGCTCTCCCTCGGCGACTCCATCTGGTCTCTCCCTCCG 141
Qy      161 ACCGATACAGACCTCGCTTTCGCGGTGATTAACAGCGGTACAAAACCTATAAGGCC 220

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Db      142 ACCCGCGAAGCAGCGCGCTTTCGACGGGAGTACCACCACTTCTCTCCCTCCCGG 201
Qy      221 CATCCACCGATTTCAAATTTACAGCATCGCGCGTCGCGCATTTACGACTTCGACACCC 280
Db      202 CCAAGAACGCCATCGCCAAACATCAACGGCGTCGCGGAAACCTGGATGGCGGCGCTCA 261
Qy      281 AATCGCGGTCAACCGGTATCTCGCGCGCGCTTTCGAGCTCAACGGCGCTCCGTCGACT 340
Db      262 TCGGCTCCGGAAGCTCGCCTTCGCGCGCACCAAGGCGGACCGGTACAAACAGCGTCAACC 321
Qy      341 TGGCGCGGACGACAGCTTTCAGCCAAACCTCATCGGCTCGGGTATTTGACGGCGGTAA 400
Db      322 TCCCGGTGACAAACAACAACAACAGTCTACGGCGGCGCGCCCAAGATCAACAACA 381
Qy      401 GCTATGCGGTTACCCGAATGTGCAATTTGGATGCGCGCTACCGTACAACTACATCGGCA 460
Db      382 ACAAGCTCAACGCCCTTCGGGTTCAACAAGATGGGGGTTACAAACAACAGCAGCAACGGCG 441
Qy      461 AAGTCAACACTGTCAAAAACGTCGTTCCGGGGAACACTGTCGTCGGCGTGGCGGTC 516
Db      442 GCGGCAACTACGGCGCAACGGCGCGACGCTGAAGAGCTACTTCAACAAGTCGGTC 497

RESULT 8
LOCUS   CF589226 741 bp mRNA linear EST 26-SEP-2003
DEFINITION EST00F06 subtracted cDNA library of JA/BTH-treated rice leaf Oryza sativa (japonica cultivar-group) cDNA clone JBI93, mRNA sequence.
ACCESSION CF589226
VERSION   CF589226.1 GI:36355281
SOURCE   EST.
ORGANISM Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 741)
AUTHORS   Yang,Y.
TITLE     Subtracted cDNA library of JA/BTH-treated rice leaf
JOURNAL   Unpublished (2003)
COMMENT   Contact: Yinong Yang
           Plant Pathology Department
           University of Arkansas
           217 Plant Sci Bldg, Fayetteville, AR 72701, USA
           Tel: 501-575-5635
           Fax: 501 575 7601
           Email: Yiyang@uark.edu
           Seq primer: T7
           Location/Qualifiers
             1..741
             /organism="Oryza sativa (japonica cultivar-group)"
             /mol_type="mRNA"
             /cultivar="Drew (a major cultivated variety in Arkansas)"
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             /clone="JBI93"
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             /dev_stage="16-day-old rice seedling treated by JA/BTH"
             /clone_lib="Subtracted cDNA library of JA/BTH-treated rice
             leaf"
             /note="Vector: pGEM-T easy; Rice seedling leaves were
             pretreated with 0.3 mM cycloheximide (CHX) half an hour
             before treatment of 0.2 mM jasmonic acid (JA) or 0.4 mM
             benzoethiadazole (BTH). Both JA- and BTH-induced mRNAs
             were equally pooled for subtracted cDNA library
             construction"

ORIGIN

Query Match      10.2%; Score 53.6; DB 7; Length 741;
Best Local Similarity 44.5%; Pred. No. 0.00064;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy      41 CGCGCGCGCACTGCGGGAAGCGCATCCGGCTTTTACGTCCAAAGCGGCGGCGCACAG 100

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Db      59 CAGCAGCGGCATGGAGGATAGCAGCGGAGTTCTACAGTTCCAGGACCGAGCTCGCGC 118
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Db      119 TGCAGAGCGGAGCTTCTCGGCGCTCTCTCGGAGCTCCATCTGTCTCTCCCTCCG 178
QY      161 ACCGATCAACGACCTTCGCGCTTCGCGTTCGATTAACGCGCTACAAAACCTATAAGCCC 220
Db      179 ACCGCGCAACGAGCGCGCTTCGAGCGGAGTACCAACCACTCTCTCCCTCCCG 238
QY      221 CATCCACCGATTTCAAACTTTACAGCATCGGCGGCTCCGCCATTTACGACTTCGACACC 280
Db      239 CMAGAACGCATCGCAACATCAACGGCTTCGCGAAACCTGGATGGCCGCGCTCA 298
QY      281 AATCGCCCGTCAACCGCTATCTCGGCGCGCTTCGAGCCTCAACCGCGCTCCGTGACT 340
Db      299 TCGGCTCGGCAAGCTTCGCTTCGCGGCCACCAAGCGCGCTACACAGCGTCAACC 358
QY      341 TGGCGGAGCGACGACTTCAGCAACCTCCATCGGCTTCGCGCTTCGCGCTTCGCGGCTAA 400
Db      359 TCCCGCTGACACAAACAAACAAAGTCTCTACGCGCGCGCGCGCAAGATCAACAACA 418
QY      401 GCTATCGCGTTACCCCGATGTCGATTTGATGCGCGCTACCGCTACAACTACATCGGCA 460
Db      419 ACACGCTCAACGCTTCGCGGTTCAACAGATGGGGGTTTACAAACAGACGACGCGG 478
QY      461 AAGTCAACACTGTCAAAAACGTCGTTCCGCGCAACTGTCGCTCGCGCTCGCGGTC 516
Db      479 GCGGCAACTACGCGGCAACGCGCGGCGAGTGAAGAGCTACTTCAACAAGTCGGTC 534

RESULT 9
CB671800
LOCUS
DEFINITION
  OSJNEe05117.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA
  clone OSJNEe05117 5', mRNA sequence.
CB671800
ACCESSION
  CB671800.1 GI:29675525
VERSION
  1 (bases 1 to 759)
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 759)
  Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
  Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
  Large-scale identification of ESTs involved in the interaction
  between rice and Magnaporthe grisea
  Unpublished (2003)
  Arizona Genomics Institute
  University of Arizona
  Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
  85721-0088, USA
  Tel: 520 626 3967
  Fax: 520 621 9288
  Email: http://genome.arizona.edu
PCR Primers
  FORWARD: gta aac cga cgg cca gtc
  BACKWARD: gga aac agc tat gac cat g
  Plate: 05 row: 1 column: 17
  Seq primer: gta aac cga cgg cca gtc.
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    /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
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Query Match
Best Local Similarity 10.2%; Score 53.6; DB 6; Length 759;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY      41 CGGCGCGGCTCGGGAAGCGCATCGGCTTTTACGTCCAAAGCGGATCGGCACAG 100
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QY      101 CAAAAGCCTCAAGCTCTTTAGTTCTGCGCAAGGCTTCAGCCGCGCTTCGCGAGGT 160
Db      95 TGCAGACGCGAGCTTCTCGGCGCTCTCTCGGAGCTCCATCTGTCTCTCCCTCCG 154
QY      161 ACCGATCAACGACCTTCGCGCTTCGCGTTCGATTAACGCGCTACAAAACCTATAAGCCC 220
Db      155 ACCGCGCAACGAGCGCGCTTCGAGCGGAGTACCAACCACTCTCTCCCTCCCG 214
QY      221 CATCCACCGATTTCAAACTTTACAGCATCGGCGGCTCCGCCATTTACGACTTCGACACC 280
Db      215 CCAAGAACGCCATCGCAACATCAACGGCTTCGCGGAAACCTGGATGGCCGCGCTCA 274
QY      281 AATCGCCCGTCAACCGCTATCTCGGCGCGCTTCGAGCCTCAACCGCGCTTCGCGCT 340
Db      275 TCGGCTCGGCAAGCTTCGCGCTTCGCGGCCACCAAGCGCGCTACAAACAGCGTCAACC 334
QY      341 TGGGCGGAGCGACGACTTCAGCAACCTCCATCGGCTTCGCGCTTCGCGGCTAA 400
Db      335 TCCCGCTGACACAAACAAACAAAGTCTCTACGCGCGCGCGCGCAAGATCAACAACA 394
QY      401 GCTATCGCGTTACCCCGATGTCGATTTGATGCGCGCTACCGCTACAACTACATCGGCA 460
Db      395 ACACGCTCAACGCTTCGCGGTTCAACAGATGGGGGTTTACAAACAGACGACGCGG 454
QY      461 AAGTCAACACTGTCAAAAACGTCGTTCCGCGCAACTGTCGCTCGCGCTCGCGGTC 516
Db      455 GCGGCAACTACGCGGCAACGCGCGGCGAGTGAAGAGCTACTTCAACAAGTCGGTC 510

RESULT 10
CB677339
LOCUS
DEFINITION
  OSJNEe14C19.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA
  clone OSJNEe14C19 5', mRNA sequence.
CB677339
ACCESSION
  CB677339.1 GI:29681064
VERSION
  1 (bases 1 to 762)
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 762)
  Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
  Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
  Large-scale identification of ESTs involved in the interaction
  between rice and Magnaporthe grisea
  Unpublished (2003)
  Arizona Genomics Institute
  University of Arizona
  Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
  85721-0088, USA
  Tel: 520 626 3967
  Fax: 520 621 9288
  Email: http://genome.arizona.edu
PCR Primers
  FORWARD: gta aac cga cgg cca gtc
  BACKWARD: gga aac agc tat gac cat g
  Plate: 14 row: C column: 19

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ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE     1 (bases 1 to 778)
AUTHORS      Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
              Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE        Large-scale identification of ESTs involved in the interaction
              between rice and Magnaporthe grisea
JOURNAL       Unpublished (2003)
COMMENT       Contact: Rod Wing
              Arizona Genomics Institute
              University of Arizona
              Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
              85721-0088, USA
              Tel: 520 626 3967
              Fax: 520 621 9288
              Email: http://genome.arizona.edu
PCR PRIMERS  FORWARD: gta aaa cga cgg cca gtc
              BACKWARD: gga aac agc tat gac cat g
              Plate: 07 row: G column: 20
              Seq primer: gta aaa cga cgg cca gtc.
              Location/Qualifiers
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              /clone_lib="OSJNEC"
              /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
              XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

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Query Match      10.2%; Score 53.6; DB 6; Length 778;
Best Local Similarity 44.5%; Pred. No. 0.00065;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

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Db 48 CAGCAGCGGCATGGAGGATACGACCGCGAGTTCTACCAAGTTTCAGCAGCAGCTCGGC 107
QY 101 CAAAACCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCGCGCATCTCGGAGGCT 160
Db 108 TGCAGACGGGAGCTTCTCGGGCTCTCCCTCGGCGACTCCATCTGCTCTCCCTCGC 167
QY 161 ACCGCATCAACGACCTTCGCTTCGCGTCGATTACACGGGCTACAAAACCTATAAGCCCC 220
Db 168 ACCGCGCAACGAGCGCGCTTCGACGGGAGTACCAACCACTTCTCTCCCTCCCGCG 227
QY 221 CATCCACGATTTCAAACTTTACAGCATCGGGCGTTCGGCCATTACGACTTCGACACCC 280
Db 228 CCAAGAACGCGCATCGCAACATCAACGGGCTCGCCGGAACCTTGGATGCCCGGCTCA 287
QY 281 AATCGCCCGTCAACACGTATCTCGGCGCGGCTTGAGCCTCAACCGCGCTTCGCTCGACT 340
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QY 341 TGGCGCGCAGCGACGCTTCAGCAAACTTCATCGGCTTCGGCGCTATTCAGCGGGCTAA 400
Db 348 TCCCGCTGACAAACAAACAAACAAAGTCTCTACGGCGCGCGCCAAAGATCAACAA 407
QY 401 GCTATCGCGTTACCCGAATGTCGATTTGGATGCGCGCTACCGCTACAACTACATCGCA 460
Db 408 ACAACGTCAACGCTTCGCGTTTCAACAAGATGGGGGTTTACAACAACGACGACGCGG 467
QY 461 AAGTCAACACTGTCAAAAACGTCGCTTCGGCGCAACTGTTCGCGCGGCTCGCGGTC 516
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RESULT 13

CB665147

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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/cultivar="Nipponbare"

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/clone="OSJNEC07G20"

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/dev_stage="3 week"

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Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

Db

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Db 71 CAGCAGCGCCATGAGGAGATACGACCGGAGTTCTACCGATTACGACCCAGCTGCGGC 130
QY 101 CAAAAGCCTCAAGCTTTTGGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCGAGCT 160
Db 131 TCGACGCGGAGCTTCTCCGGCTCTCCCTCGGAGCTCCATCTGGTCTTCCCTCCCTCGG 190
QY 161 ACCGATCAACGACCTCCGCTTCGCGTTCGATTACACGCGCTACAAAACTATAAGCCC 220
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Db 311 TCGGCTCCGGCAAGCTCGGCTTCGGGCGCCACCAAGGCGACCGCTACACGCGTCAACC 370
QY 341 TGGGCGGCGACGACAGCTTCAGCCAAACCTCCATCGGCTTCGGCGTATTGACGGGCGTAA 400
Db 371 TCCCGCTCGACAAACAAACAAAGTCTACGCGGCGCGCCAAAGATCAACAACA 430
QY 401 GCTATGCGGTACCCCGAATGTCGATTTGGATGCCGCTACCGCTACACTACATCGGCA 460
Db 431 ACAACGTCAACCGCTTCGGGTTCAACAGATGGGGGGTTACAAACACACGACGACGCGG 490
QY 461 AAGTCAACACTGTCAAAAAACGTCCGTTCCGGGAACTGTCCGTCGGCGTGC 511
Db 491 GCGGCAACGCGCGGACGTGAGAGCTACTTCAACAAAGTCGGTCGGGAGGC 541

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Job time : 7711 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2005, 19:34:43 ; Search time 302 Seconds
(without alignments)
222.835 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868

Sequence: 1 MKKALATLIALPALPAALAE.....VNTVKRSGELSGVRVKF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	2	Aaw04891 Proteinase
2	868	100.0	174	6	Abu79079 N. mening
3	868	100.0	174	7	Adf43316 N. mening
4	868	100.0	174	8	Adl16114 Neisseria
5	868	100.0	174	8	Adl13428 Neisseria
6	868	100.0	174	8	Adl24352 N meningi
7	864	99.5	174	8	Adp08236 Neisseria
8	857	98.7	174	8	Adl24383 N meningi
9	854	98.4	174	2	Aaw04893 Proteinase
10	825	95.0	174	2	Aaw04894 Proteinase
11	825	95.0	174	5	Abg91063 Neisseria
12	824.5	95.0	175	2	Aaw04892 Proteinase
13	820	94.5	166	8	Adl24385 N meningi
14	809.5	93.3	175	6	Abp77991 N. gonorr
15	794	91.5	162	8	Adl24387 N meningi
16	793	91.4	162	8	Adl24386 N meningi
17	785	90.4	155	4	Aab19895 Neisseria
18	781	90.0	155	8	Adl13426 Neisseria
19	779.5	89.8	161	8	Adl24384 N meningi
20	746	85.9	154	8	Adl24388 N meningi
21	657.5	75.7	141	8	Adl24389 N meningi
22	234	27.0	208	5	Aao17579 M catarrh
23	224	25.8	232	6	Abp79561 N. gonorr
24	221.5	25.5	176	5	Aau97605 Haemophil
25	221.5	25.5	176	5	Aau97603 Haemophil

26	221.5	25.5	176	5	AAU97602	Haemophil
27	221.5	25.5	176	5	AAU97604	Haemophil
28	218.5	25.2	229	6	ABP79854	N. gonorr
29	218	25.1	226	6	ABP79754	N. gonorr
30	214.5	24.7	176	5	AAU97601	Haemophil
31	214	24.7	281	6	ABP80738	N. gonorr
32	212	24.4	278	6	ABP80098	N. gonorr
33	210	24.2	265	6	ABP77624	N. gonorr
34	207.5	23.9	186	6	ABP80662	N. gonorr
35	206	23.7	278	6	ABP80428	N. gonorr
36	204.5	23.6	229	6	ABP77612	N. gonorr
37	194.5	22.4	227	6	ABP77150	N. gonorr
38	194.5	22.4	227	6	ABP76762	N. gonorr
39	178	20.5	189	6	ABP78327	N. gonorr
40	141	16.2	27	8	ADL27222	Peptide f
41	135	15.6	170	2	AAW73911	Neisseria
42	133	15.3	25	2	AAW04912	N. mening
43	132	15.2	28	8	ADL27223	Peptide f
44	126.5	14.6	201	8	ADP08324	Neisseria
45	122.5	14.1	94	8	ADT05699	Haemophil

ALIGNMENTS

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ID AAW04891 standard; protein; 174 AA.
XX AAW04891;
XX XX
DT 16-OCT-2003 (revised)
DT 22-DEC-1996 (first entry)
XX XX
DE Proteinase K resistant N. meningitidis 22 kD surface protein.
XX XX
KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
KW antibody; detection; probe; surface protein.
XX XX
OS Neisseria meningitidis; strain 608B.
XX XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= sig_peptide 20..174
FT FT /label= mat_protein
XX XX
PN WO9629412-A1.

XX XX
XX 26-SEP-1996.
XX XX
PF 15-MAR-1996; 96WO-CA000157.
XX XX
PR 17-MAR-1995; 95US-00406362.
XX XX
PR 04-AUG-1995; 95US-0001983P.
XX XX
PA (IAFB-) IAF BIO VAC INC.
XX XX
PI Brodeur BR, Martin D, Hamel J, Rioux C;
XX XX
DR WPI; 1996-443187/44.
XX XX
N-PSDB; AAT39039.
XX XX
PT Neisseria meningitidis antigen, highly conserved between different
PT strains - useful for prodn. of antibodies for immunisation against, or
XX diagnosis of, N. meningitidis infection.
XX XX
PS Claim 7; Fig 1; 117pp; English.

XX CC
A proteinase K resistant surface protein has been isolated from 4 strains
XX CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
XX CC antigenic fragments of antibodies can be used in a vaccine for the
XX CC prevention of infection by N. meningitidis or by N. gonorrhoeae in

CC humans. The antibodies may also be used diagnostically to detect N.
 CC meningitidis infection. The antigen may also be used to detect antibodies
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,
 CC or their fragments, can be used as probes for the detection of pathogenic
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
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 SQ Sequence 174 AA;
 Query Match 100.0%; Score 868; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 9.3e-87;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGSDSF 120
 QY 121 SQTSLGLVLTGVSVAVTNPVLDAGRYNYIGKNTVKNVRSGLSVGVVRKF 174
 DB 121 SQTSLGLVLTGVSVAVTNPVLDAGRYNYIGKNTVKNVRSGLSVGVVRKF 174
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 ABU79079
 ID ABU79079 standard; protein; 174 AA.
 AC ABU79079;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE N. meningitidis lipopolysaccharide protein.
 XX
 XN Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; energy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.
 XX
 OS Neisseria meningitidis.
 XX
 PN US2002177551-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 30-MAY-2001; 2001US-00870759.
 XX
 PR 31-MAY-2000; 2000US-0208128P.
 XX
 PA (TERM/) Terman D S.
 XX
 PI Terman DS;
 XX
 XX WPI; 2003-361759/34.
 DR N-PSDB; ACA64711.
 XX
 PT A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces energy or apoptosis
 PT in T cells and antigen presenting cells.
 XX
 PS Disclosure; Page; 167pp; English.
 XX
 CC The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidally
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing which
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents an anti-tumour protein which is co-administered with
 CC or incorporated into a fusion construct with a superantigen. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from the US patent
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 SQ Sequence 174 AA;
 Query Match 100.0%; Score 868; DB 6; Length 174;
 Best Local Similarity 100.0%; Pred. No. 9.3e-87;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGSDSF 120
 QY 121 SQTSLGLVLTGVSVAVTNPVLDAGRYNYIGKNTVKNVRSGLSVGVVRKF 174
 DB 121 SQTSLGLVLTGVSVAVTNPVLDAGRYNYIGKNTVKNVRSGLSVGVVRKF 174
 RESULT 3
 ADP43316
 ID ADP43316 standard; protein; 174 AA.
 XX
 AC ADP43316;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE N. meningitidis lipopolysaccharide seq id 36.
 XX
 XN receptor; lipid-based tumour associated antigen; cytostatic;
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
 KW infectious disease; lipopolysaccharide; LPS.
 XX

OS Neisseria meningitidis.
 PN US2003157113-A1.
 XX
 PD 21-AUG-2003.
 XX
 PF 28-DEC-2000; 2000US-00751708.
 XX
 PR 28-DEC-1999; 99US-0173371P.
 XX
 PA (TERM/) Terman D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 2003-787326/74.
 DR N-PSDB; ADF43315.
 XX
 PT New receptor in a mammalian cell that inhibits regular activation by
 PT receptors specific for lipid-based tumor associated antigens, useful for
 PT treating a neoplastic disease or tumor, and infectious diseases.
 XX
 PS Disclosure; SEQ ID NO 36; 151pp; English.
 XX
 CC The invention describes a receptor in a mammalian cell that inhibits
 CC regular activation by receptors specific for lipid-based tumor
 CC associated antigen. The receptor has cytostatic and antimicrobial
 CC properties and is suitable for use in gene therapy. The receptors,
 CC methods and compositions are useful for treating a neoplastic disease or
 CC tumor (cancer), and infectious diseases. This is the amino acid sequence
 CC of Neisseria meningitidis lipopolysaccharide (LPS) to which tumor cells
 CC develop immunity.
 XX
 SQ Sequence 174 AA;
 Query Match 100.0%; Score 868; DB 7; Length 174;
 Best Local Similarity 100.0%; Pred. No. 9.3e-87;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNARSVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNARSVDLGGSDSF 120
 QY 121 SQTSLGLGVLTCGVSYAVTPNVLDAGYRNYIGKVTNKNRSGELSGVRVKF 174
 DB 121 SQTSLGLGVLTCGVSYAVTPNVLDAGYRNYIGKVTNKNRSGELSGVRVKF 174
 RESULT 4
 ADL16114
 ID ADL16114 standard; protein; 174 AA.
 XX
 AC ADL16114;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Neisseria meningitidis NspA for use in vaccine.
 XX
 KW Outer membrane vesicle preparation; OMV; detergent-free;
 KW physical disruption; vaccine; serogroup B; NspA;
 KW Neisserial surface protein A; immunogen.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO2004019977-A2.
 XX
 PD 11-MAR-2004.
 XX
 PF 01-SEP-2003; 2003WO-IB004293.
 XX

PR 30-AUG-2002; 2002GB-00020194.
 XX
 PA (CHIR) CHIRON SRL.
 XX
 PI Pizza M, Serruto D, Rappuoli R;
 XX
 DR WPI; 2004-239124/22.
 XX
 PT Producing an outer membrane vesicle (OMV) preparation from a bacterium,
 PT useful as a vaccine against Neisseria meningitidis serogroup B, comprises
 PT disrupting the bacterial membrane in the absence of deoxycholate
 PT detergent.
 XX
 PS Disclosure; Fig 3; 20pp; English.
 XX
 CC The invention relates to a process for producing an outer membrane
 CC vesicle (OMV) preparation from a bacterium. The process involves
 CC disrupting the bacterial membrane substantially in the absence of
 CC deoxycholate detergent or other detergent, followed by several
 CC centrifugation steps. Membrane disruption is achieved by sonication,
 CC homogenisation, microfluidisation, cavitation, osmotic shock, grinding,
 CC French press, belnding or any other physical technique. The outer
 CC membrane vesicles can be prepared from bacteria of the genera Moraxella,
 CC Shigella, Pseudomonas, Treponema, Porphyromonas, Helicobacter or
 CC Neisseria, and are particularly produced from Neisseria meningitidis
 CC (especially serogroup B) or Neisseria gonorrhoeae. The invention also
 CC relates to a Neisseria meningitidis outer membrane vesicle composition in
 CC which the vesicles include the immunogens NspA (Neisserial surface
 CC protein A; ADL16114), 287 protein (ADL16113) and 741 protein (ADL16112);
 CC and the use of outer membrane vesicle compositions as a medicament,
 CC especially for raising an immune response in a patient. The method is
 CC useful for manufacturing an outer membrane vesicle preparation as a
 CC vaccine against Neisseria meningitidis serogroup B. The present sequence
 CC represents Neisseria meningitidis NspA.
 XX
 SQ Sequence 174 AA;
 Query Match 100.0%; Score 868; DB 8; Length 174;
 Best Local Similarity 100.0%; Pred. No. 9.3e-87;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNARSVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNARSVDLGGSDSF 120
 QY 121 SQTSLGLGVLTCGVSYAVTPNVLDAGYRNYIGKVTNKNRSGELSGVRVKF 174
 DB 121 SQTSLGLGVLTCGVSYAVTPNVLDAGYRNYIGKVTNKNRSGELSGVRVKF 174
 RESULT 5
 ADL13428
 ID ADL13428 standard; protein; 174 AA.
 XX
 AC ADL13428;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Neisseria meningitidis H44/76 full-length NspA protein.
 XX
 KW Neisserial surface protein A; NspA; refolding; recombinant production;
 KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;
 KW invasive bacterial disease; bacteraemia; meningitis;
 KW Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;
 KW antibacterial; gene therapy.
 XX
 OS Neisseria meningitidis; H44/76.
 XX
 PF Key Location/Qualifiers
 XX

```

FT Peptide 1. .19
FT /label= Signal_peptide
FT Protein 20. .174
FT /label= Mature_NspA
FT Misc-difference 168
FT /note= "The corresponding residue in the mature protein
FT shown in Fig 2 (residue 149) is Ala"
XX
XX
XX
XX WO2004020452-A2.
XX
XX PD 11-MAR-2004.
XX
XX PF 28-AUG-2003; 2003WO-EP010085.
XX
XX PR 30-AUG-2002; 2002GB-00020197.
XX
XX (GLAX ) GLAXOSMITHKLINE BIOLOGICALS SA.
XX (UYUT-) RIJKSUNIV UTRECHT.
XX
XX Biemans R, Bos M, Denoel P, Peron C, Goraj K, Poolman J;
XX Tommassen J, Weynants V;
XX
XX WPI; 2004-239150/22.
XX N-PSDB; ADL13427.
XX
XX New refolded NspA protein, useful for preparing a composition for
XX diagnosing, treating or preventing infection caused by Neisseria
XX meningitidis or Neisseria gonorrhoeae.
XX
XX Disclosure; Fig 3; 62pp; English.
XX
XX The invention relates to an isolated refolded Neisserial surface protein
XX A (NspA) from Neisseria meningitidis or Neisseria gonorrhoeae. The
XX invention also relates to the method of refolding an NspA protein; an
XX alkaline refolding buffer comprising ethanolamine and SB-12 (3-
XX dimethylododecylammonio)propanesulphonate) for refolding an NspA protein; a
XX pharmaceutical composition comprising the refolded NspA protein, a
XX carrier and optionally one or more other Neisserial antigens; a method of
XX preventing or treating a Neisserial infection; an antibody immunospecific
XX for the NspA protein; and diagnosing a Neisserial infection. NspA has
XX characteristics which indicate that it is a potential vaccine candidate
XX for the development of subunit vaccines for the treatment of infections
XX caused by Neisseria meningitidis (meningococcus), which causes invasive
XX bacterial diseases such as bacteraemia and meningitis, or Neisseria
XX gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced
XX NspA could therefore be used to produce vaccine compositions and it could
XX also be used in the development of new antimicrobial agents, diagnostic
XX tests and in drug screening. However, recombinantly produced proteins are
XX frequently unable to adopt their biologically active conformations, and
XX yields may be very low due to mis-folding and aggregation of the protein.
XX The method of the invention provides an improved method for refolding the
XX NspA protein, and it is possible to increase the recovery of active
XX protein form partly purified inclusion bodies in amounts up to 100%
XX without the need for further purification. The refolded NspA protein is
XX useful for preparing a composition for diagnosing, treating or preventing
XX infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The
XX present sequence represents the full-length NspA protein from Neisseria
XX meningitidis H44/76.
XX
XX SQ Sequence 174 AA;
XX
XX Query Match 100.0%; Score 868; DB 8; Length 174;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-87;
XX Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGSPRISAGYRINDLR 60
XX
XX 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGSPRISAGYRINDLR 60
XX
XX 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSF 120
XX
XX 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSF 120
XX
XX 121 SOTSIGLGLVTGVSVAVTENVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
XX
XX 121 SOTSIGLGLVTGVSVAVTENVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174

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QY 121 SOTSIGLGLVTGVSVAVTENVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
DB 121 SOTSIGLGLVTGVSVAVTENVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174

RESULT 6
ID ADL24352
XX ADL24352 standard; protein; 174 AA.
XX
XX AC ADL24352;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE N meningitidis strain 608B NspA protein.
XX
XX KW NspA; vaccine; antibacterial; meningitis.
XX
XX OS Neisseria meningitidis.
XX
XX PN WO2004019976-A2.
XX
XX PD 11-MAR-2004.
XX
XX PF 29-AUG-2003; 2003WO-CA001452.
XX
XX PR 30-AUG-2002; 2002US-0406980P.
XX
XX PA (SHIR-) SHIRE BIOCHEM INC.
XX
XX PI Martin D, Rioux S;
XX
XX DR WPI; 2004-239123/22.
XX N-PSDB; ADL24351.
XX
XX Composition comprising liposome associated with isolated polypeptide or
XX polynucleotide derived from Neisseria meningitidis strain 608B, or its
XX fragment or analog, useful for inducing an immune response against N.
XX meningitidis.
XX
XX Claim 1; Fig 1; 79pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX a liposome associated with an isolated polypeptide derived from Neisseria
XX meningitidis strain 608B, where the polypeptide is the NspA protein. The
XX composition is useful for inducing an immune response against N.
XX meningitidis, for preventing and/or treating N. meningitidis infection
XX and for treating and/or preventing neisserial infection chosen from N.
XX meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharaea. It is
XX useful for treatment or prophylaxis of meningitis and meningococcaemia, in
XX a host. The host is a mammal, preferably a human and more preferably an
XX adult human. The present sequence is the Neisseria meningitidis strain
XX 608B NspA protein.
XX
XX SQ Sequence 174 AA;
XX
XX Query Match 100.0%; Score 868; DB 8; Length 174;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-87;
XX Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGSPRISAGYRINDLR 60
XX
XX 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGSPRISAGYRINDLR 60
XX
XX 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSF 120
XX
XX 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSF 120
XX
XX 121 SOTSIGLGLVTGVSVAVTENVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
XX
XX 121 SOTSIGLGLVTGVSVAVTENVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174

RESULT 7

```

ADP08236
 ID ADP08236 standard; protein; 174 AA.
 XX
 AC ADP08236;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Neisseria meningitidis MC58 OMV-related membrane protein - SEQ ID 69.
 XX
 KW outer-membrane vesicle; antibacterial; antiinflammatory;
 KW meningococcal protein trafficking; localisation; infection; vaccine;
 KW gene therapy.
 XX
 OS Neisseria meningitidis MC58.
 XX
 PN WO2004046177-A2.
 XX
 PD 03-JUN-2004.
 XX
 PF 17-NOV-2003; 2003WO-IB006281.
 XX
 PR 15-NOV-2002; 2002GB-00026734.
 PR 27-MAR-2003; 2003GB-00007131.
 XX
 PA (CHIR) CHIRON SRL.
 XX
 PI Norais N, Grandi G;
 XX
 DR WPI; 2004-420615/39.
 XX
 PT New compositions having outer-membrane vesicles and proteins from
 PT Neisseria meningitidis, useful in the field of meningococcal
 PT biochemistry, in particular for preventing and/or treating meningococcal
 PT infections.
 XX
 PS Claim 9; SEQ ID NO 69; 79pp; English.
 XX
 CC The invention relates to a novel composition comprising outer-membrane
 CC vesicles (OMV) prepared from a first strain of Neisseria meningitidis and
 CC 1 or more proteins which are present in OMVs prepared from a second
 CC strain of N. meningitidis, but which are not present in OMVs prepared
 CC from the first strain. The composition of the invention demonstrates
 CC antibacterial and antiinflammatory activities and may be useful in the
 CC field of meningococcal biochemistry, in particular the trafficking and
 CC localisation of meningococcal proteins, as well as in the prevention or
 CC treatment of meningococcal infections, possibly via the production of a
 CC vaccine or gene therapy. The current sequence is that of a Neisseria
 CC meningitidis MC58 outer-membrane vesicle (OMV)-related membrane protein
 CC of the invention.
 XX
 SQ Sequence 174 AA;
 Query Match 99.5%; Score 864; DB 8; Length 174;
 Best Local Similarity 99.4%; Pred. No. 2.5e-86;
 Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVLDGGSDF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVLDGGSDF 120
 QY 121 SQTSLGLGLTGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
 DB 121 SQTSLGLGLTGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
 RESULT 8
 ID ADL24383
 ID ADL24383 standard; protein; 174 AA.
 XX

AC ADL24383;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE N meningitidis strain 608B modified NspA protein #1.
 XX
 KW mutein; mutant; NspA; vaccine; antibacterial; meningitis.
 XX
 OS Neisseria meningitidis.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 115 /note= "wild-type Gly substituted by Ala"
 FT Misc-difference 118 /note= "wild-type Asp substituted by Asn"
 FT
 XX
 PN WO2004019976-A2.
 XX
 PD 11-MAR-2004.
 XX
 PF 29-AUG-2003; 2003WO-CA001452.
 XX
 PR 30-AUG-2002; 2002US-0406980P.
 XX
 PA (SHIR-) SHIRE BIOCHEM INC.
 XX
 PI Martin D, Rioux S;
 XX
 DR WPI; 2004-239123/22.
 XX
 PT Composition comprising liposome associated with isolated polypeptide or
 PT polynucleotide derived from Neisseria meningitidis strain 608B, or its
 PT fragment or analog, useful for inducing an immune response against N.
 PT meningitidis.
 XX
 PS *Example 4; Page; 79pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition comprising
 CC a liposome associated with an isolated polypeptide derived from Neisseria
 CC meningitidis strain 608B, where the polypeptide is the NspA protein. The
 CC composition is useful for inducing an immune response against N.
 CC meningitidis, for preventing and/or treating N. meningitidis infection
 CC and for treating and/or preventing neisserial infection chosen from N.
 CC meningitidis, N. gonorrhoeae, N. lactamica and N. polysacchara. It is
 CC useful for treatment or prophylaxis of meningitis and meningococemia, in
 CC a host. The host is a mammal, preferably a human and more preferably an
 CC adult human. The present sequence is a modified version of the Neisseria
 CC meningitidis strain 608B NspA protein. Note: This sequence is not shown
 CC in the specification but has been created based on the information given
 CC and the wild-type NspA protein shown in Figure 1.
 XX
 SQ Sequence 174 AA;
 Query Match 98.7%; Score 857; DB 8; Length 174;
 Best Local Similarity 98.9%; Pred. No. 1.5e-85;
 Matches 172; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVLDGGSDF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVLDGGSDF 120
 QY 121 SQTSLGLGLTGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
 DB 121 SQTSLGLGLTGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
 RESULT 9
 ID AAW04893

ID	AAW04893 standard; protein; 174 AA.	ID	AAW04894 standard; protein; 174 AA.
XX	AAW04893;	XX	AAW04894;
AC		AC	
XX		XX	
DT	16-OCT-2003 (revised)	DT	16-OCT-2003 (revised)
DT	22-DEC-1996 (first entry)	DT	22-DEC-1996 (first entry)
XX		XX	
DE	Proteinase K resistant N. meningitidis 22 kD surface protein.	DE	Proteinase K resistant N. meningitidis 22 kD surface protein.
XX		XX	
KW	Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;	KW	Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
KW	antibody; detection; probe; surface protein.	KW	antibody; detection; probe; surface protein.
XX		XX	
OS	Neisseria meningitidis; strain Z4063.	OS	Neisseria meningitidis; strain b2.
XX		XX	
FH	Key Location/Qualifiers	FH	Key Location/Qualifiers
FT	Peptide 1..19	FT	Peptide 1..19
FT	/label= sig_peptide	FT	/label= sig_peptide
FT	Protein 20..174	FT	Protein 20..174
FT	/label= mat_protein	FT	/label= mat_protein
XX		XX	
PN	WO9629412-A1.	PN	WO9629412-A1.
XX		XX	
PD	26-SEP-1996.	PD	26-SEP-1996.
XX		XX	
PF	15-MAR-1996; 96WO-CA000157.	PF	15-MAR-1996; 96WO-CA000157.
XX		XX	
PR	17-MAR-1995; 95US-00406362.	PR	17-MAR-1995; 95US-00406362.
PR	04-AUG-1995; 95US-0001983P.	PR	04-AUG-1995; 95US-0001983P.
XX		XX	
PA	(IAPB-) IAF BIO VAC INC.	PA	(IAPB-) IAF BIO VAC INC.
XX		XX	
PI	Brodeur BR, Martin D, Hamel J, Rioux C;	PI	Brodeur BR, Martin D, Hamel J, Rioux C;
XX		XX	
DR	WPI; 1996-443187/44.	DR	WPI; 1996-443187/44.
DR	N-PSDB; AAT39041.	DR	N-PSDB; AAT39042.
XX		XX	
PT	Neisseria meningitidis antigen, highly conserved between different	PT	Neisseria meningitidis antigen, highly conserved between different
PT	strains - useful for prodn. of antibodies for immunisation against, or	PT	strains - useful for prodn. of antibodies for immunisation against, or
PT	diagnosis of, N. meningitidis infection.	PT	diagnosis of, N. meningitidis infection.
XX		XX	
PS	Claim 7; Fig 9; 117pp; English.	PS	Claim 7; Fig 10; 117pp; English.
XX		XX	
CC	A proteinase K resistant surface protein has been isolated from 4 strains	CC	A proteinase K resistant surface protein has been isolated from 4 strains
CC	of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,	CC	of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
CC	antigenic fragments of antibodies can be used in a vaccine for the	CC	antigenic fragments of antibodies can be used in a vaccine for the
CC	prevention of infection by N. meningitidis or by N. gonorrhoeae in	CC	prevention of infection by N. meningitidis or by N. gonorrhoeae in
CC	humans. The antibodies may also be used diagnostically to detect N.	CC	humans. The antibodies may also be used diagnostically to detect N.
CC	meningitidis infection. The antigen may also be used to detect antibodies	CC	meningitidis infection. The antigen may also be used to detect antibodies
CC	specific to N. meningitidis antigen. DNA sequences encoding the antigen,	CC	specific to N. meningitidis antigen. DNA sequences encoding the antigen,
CC	or their fragments, can be used as probes for the detection of pathogenic	CC	or their fragments, can be used as probes for the detection of pathogenic
CC	Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)	CC	Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
XX		XX	
SQ	Sequence 174 AA;	SQ	Sequence 174 AA;
<p>Query Match 98.4%; Score 854; DB 2; Length 174; Best Local Similarity 98.3%; Pred. No. 3.2e-85; Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>		<p>Query Match 95.0%; Score 825; DB 2; Length 174; Best Local Similarity 94.3%; Pred. No. 4.8e-82; Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;</p>	
QY	1 MKKALATLALPAALAEAGSGFVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60	QY	1 MKKALATLALPAALAEAGSGFVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db	1 MKKALATLALPAALAEAGSGFVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60	Db	1 MKKALATLALPAALAEAGSGFVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120	QY	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
Db	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120	Db	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
QY	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSSELSVGVRVKF 174	QY	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSSELSVGVRVKF 174
Db	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSSELSVGVRVKF 174	Db	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSSELSVGVRVKF 174
<p>RESULT 10 AAW04894</p>		<p>RESULT 11 ABG91063</p>	

ID ABG91063 standard; protein; 174 AA.
 AC ABG91063;
 XX
 XX
 XX 29-NOV-2002 (first entry)
 DE Neisseria gonorrhoeae outer membrane protein #1.
 XX
 XX Gran-negative bacterial bleb; PorB; outer membrane protein;
 KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
 KW protective antigen; antibacterial; vaccine.
 XX
 XX Neisseria gonorrhoeae.
 OS
 PN WO200262380-A2.
 XX
 XX 15-AUG-2002.
 PD
 XX
 XX 08-FEB-2002; 2002WO-EP001356.
 PF
 XX 08-FEB-2001; 2001GB-00003169.
 XX
 PR (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PA Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;
 XX
 PI WPI; 2002-657510/70.
 XX
 DR N-PSDB; ABS67381.
 DR
 XX Novel gram-negative bacterial bleb presenting on its surface PorB outer
 PT membrane protein from Chlamydia trachomatis or protective antigen from
 PT Chlamydia pneumoniae; useful for preventing Chlamydia infection.
 XX
 XX Disclosure; Page 54; 75pp; English.
 PS
 XX The present invention relates to a new gram-negative bacterial bleb
 CC presenting on its surface the PorB outer membrane protein from Chlamydia
 CC trachomatis, or a protective antigen from C. pneumoniae. The invention is
 CC useful for preventing C. trachomatis or C. pneumoniae infection in a
 CC host. The present amino acid sequence represents a Neisseria gonorrhoeae
 CC protein as described in the invention
 XX
 XX Sequence 174 AA;
 SQ
 Query Match 95.0%; Score 825; DB 5; Length 174;
 Best Local Similarity 94.3%; Pred. No. 4.8e-82;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALAALIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVLDGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVLDGSDSF 120
 QY 121 SOTSIGLGLGVTSYAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
 DB 121 SKTSAGLGLGVTSYAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
 RESULT 12
 AAW04892
 ID AAW04892 standard; protein; 175 AA.
 XX
 XX AAW04892;
 XX
 XX 16-OCT-2003 (revised)
 DT 22-DEC-1996 (first entry)
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 XX Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;

KW antibody; detection; probe; surface protein.
 XX
 XX Neisseria meningitidis; strain MCH88.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= sig_peptide
 FT 20..175
 FT /label= mat_protein
 PN WO9629412-A1.
 XX
 XX 26-SEP-1996.
 PD
 XX 15-MAR-1996; 96WO-CA000157.
 PF
 XX 17-MAR-1995; 95US-00406362.
 PR 04-AUG-1995; 95US-0001983P.
 XX
 XX (IAFB-) IAF BIO VAC INC.
 PA
 XX Brodeur BR, Martin D, Hamel J, Rioux C;
 PI WPI; 1996-443187/44.
 DR N-PSDB; AAT39040.
 DR
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against, or
 PT diagnosis of, N. meningitidis infection.
 PT
 XX Claim 7; Fig 8; 117pp; English.
 PS
 XX A proteinase K resistant surface protein has been isolated from 4 strains
 CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
 CC antigenic fragments of antibodies can be used in a vaccine for the
 CC prevention of infection by N. meningitidis or by N. gonorrhoeae in
 CC humans. The antibodies may also be used diagnostically to detect N.
 CC meningitidis infection. The antigen may also be used to detect antibodies
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,
 CC or their fragments, can be used as probes for the detection of pathogenic
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 XX Sequence 175 AA;
 SQ
 Query Match 95.0%; Score 824.5; DB 2; Length 175;
 Best Local Similarity 95.4%; Pred. No. 5.5e-82;
 Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
 QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALAALIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVLDGSDS 119
 DB 61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDFNGSDS 120
 QY 120 FSQTSIGLGLGVTSYAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
 DB 121 FSQTSIGLGLGVTSYAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 175
 RESULT 13
 ADL24385
 ID ADL24385 standard; protein; 166 AA.
 XX
 XX ADL24385;
 XX
 XX 03-JUN-2004 (first entry)
 DT
 XX N meningitidis strain 608B modified NspA protein #3.
 DE
 XX mutein; mutant; NspA; vaccine; antibacterial; meningitis.
 KW
 XX

OS	Neisseria meningitidis.
XX	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 35..36
FT	/note= "wild-type NspA residues 36-43 deleted"
XX	
PN	WO2004019976-A2.
XX	
PD	11-MAR-2004.
XX	
PB	29-AUG-2003; 2003WO-CA001452.
XX	
PR	30-AUG-2002; 2002US-0406980P.
XX	(SHIR-) SHIRE BIOCHEM INC.
PA	Martin D, Rioux S;
PI	WPI; 2004-239123/22.
XX	
DR	Composition comprising liposome associated with isolated polypeptide or
PT	polynucleotide derived from Neisseria meningitidis strain 608B, or its
PT	fragment or analog, useful for inducing an immune response against N.
PT	meningitidis.
XX	
PS	Example 4; Page; 79pp; English.
XX	
CC	The present invention relates to a pharmaceutical composition comprising.
CC	a liposome associated with an isolated polypeptide derived from Neisseria
CC	meningitidis strain 608B, where the polypeptide is the NspA protein. The
CC	composition is useful for inducing an immune response against N.
CC	meningitidis, for preventing and/or treating N. meningitidis infection
CC	and for treating and/or preventing neisserial infection chosen from N.
CC	meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharaea. It is
CC	useful for treatment or prophylaxis of meningitis and meningococcalemia, in
CC	a host. The host is a mammal, preferably a human and more preferably an
CC	adult human. The present sequence is a modified version of the Neisseria
CC	meningitidis strain 608B NspA protein. Note: This sequence is not shown
CC	in the specification but has been created based on the information given
CC	and the wild-type NspA protein shown in Figure 1.
XX	
SQ	Sequence 166 AA;
	Query Match 94.5%; Score 820; DB 8; Length 166;
	Best Local Similarity 95.4%; Pred. No. 1.6e-81;
	Matches 166; Conservative 0; Mismatches 0; Indels 8; Gaps 1
Qy	1 MKKALATLIALPALPAALAAGSGFYVQADAAHAHAKASSLSGSAKFSPRISAGYRINDLR 60
Dd	MKKALATLIALPALPAALAAGSGFYVQADAAHAHAK-----KGFSPPRISAGYRINDLR 52
Qy	61 FAVDYTRYKNVKAPSTDPKLYSIGASAIYDFTQSPVKPYLCARLSLNRAVDLGGSDSF 120
Dd	53 FAVDYTRYKNVKAPSTDPKLYSIGASAIYDFTQSPVKPYLCARLSLNRAVDLGGSDSF 112
Qy	121 QTSIGLGVLTCGSYAIVTPNVLDLAGRYNYIKGVNTKVNRSGELSGVRVKF 174
Dd	113 QTSIGLGVLTCGSYAIVTPNVLDLAGRYNYIKGVNTKVNRSGELSGVRVKF 166
RESULT 14	
ABP77991	ABP77991 standard; protein; 175 AA.
XX	AC ABP77991;
XX	
DT	07-MAR-2003 (first entry)
XX	
DE	N. gonorrhoeae amino acid sequence SEQ ID 2512.
XX	Antibacterial; infection; vaccine; gene therapy.
XX	

Search completed: May 19, 2005, 20:55:00
Job time : 304 secs

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OM protein - protein search, using sw model

Run on: May 19, 2005, 20:41:43 ; Search time 113 Seconds
(without alignments)
114.946 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868

Sequence: 1 MKKALATLIALPAALAE.....VNTKVRSGELSGVGRVKF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	868	100.0	174	3	US-08-913-362-2
2	854	98.4	174	3	US-08-913-362-6
3	838.5	96.6	175	3	US-08-913-362-30
4	825	95.0	174	3	US-08-913-362-8
5	824.5	95.0	175	3	US-08-913-362-4
6	135	15.6	170	1	US-08-127-499A-20
7	135	15.6	170	1	US-08-482-847-20
8	133	15.3	25	3	US-08-913-362-26
9	113.5	13.1	98	4	US-09-540-236-2245
10	109.5	12.6	187	4	US-09-489-039A-13699
11	104.5	12.0	384	4	US-09-543-681A-7922
12	93	10.7	190	4	US-09-543-681A-7684
13	92.5	10.7	261	4	US-09-252-991A-19759
14	89.5	10.3	186	4	US-09-540-236-2792
15	89.5	10.3	385	4	US-09-489-039A-7451
16	88.5	10.2	180	4	US-09-164-714-7
17	88.5	10.2	573	3	US-09-336-447A-3
18	88.5	10.2	573	1	US-09-952-267B-3
19	88	10.1	359	1	US-08-457-997B-2
20	88	10.1	359	3	US-08-467-722A-2
21	88	10.1	359	4	US-09-451-184-2
22	88	10.1	397	4	US-09-902-540-16267
23	88	10.1	610	3	US-09-336-447A-11
24	88	10.1	610	4	US-09-952-267B-11
25	88	10.1	624	3	US-09-336-447A-7
26	88	10.1	624	4	US-09-952-267B-7
27	88	10.1	889	3	US-09-336-447A-15

28	88	10.1	889	4	US-09-952-267B-15	Sequence 15, Appl
29	87.5	10.1	708	4	US-09-336-115C-2	Sequence 2, Appl
30	87	10.0	16	3	US-08-913-362-15	Sequence 15, Appl
31	87	10.0	500	4	US-09-325-932A-149	Sequence 149, Appl
32	86	9.9	512	4	US-09-059-584-57	Sequence 57, Appl
33	85.5	9.9	238	4	US-09-902-540-12284	Sequence 12284, A
34	85.5	9.9	487	4	US-09-328-352-5331	Sequence 5331, Ap
35	85	9.8	568	5	PCT-US95-13749-5	Sequence 5, Appl
36	84.5	9.7	643	4	US-09-328-352-5146	Sequence 5146, Ap
37	84	9.7	351	4	US-09-252-991A-30094	Sequence 30094, A
38	83.5	9.6	721	4	US-09-328-352-7781	Sequence 7781, Ap
39	83	9.6	364	4	US-09-418-980-8	Sequence 8, Appl
40	83	9.6	364	4	US-09-809-665A-151	Sequence 151, Appl
41	82	9.4	172	4	US-09-902-540-14682	Sequence 14682, A
42	82	9.4	433	2	US-08-883-515-2	Sequence 2, Appl
43	82	9.4	512	4	US-09-059-584-56	Sequence 56, Appl
44	82	9.4	867	4	US-09-540-236-2676	Sequence 2676, Ap
45	81	9.3	15	3	US-08-913-362-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-913-362-2
; Sequence 2, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001.983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 04/998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-913-362-2

Query Match 100.0%; Score 868; DB 3; Length 174;

Best Local Similarity 100.0%; Pred. No. 7.9e-93;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDTRYKKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDSF 120
DB 61 FAVDTRYKKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDSF 120

QY 121 SQTSLGLVLTGVSAYATPNDVLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174
DB 121 SQTSLGLVLTGVSAYATPNDVLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 2

US-08-913-362-6
; Sequence 6, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-913-362-6

Query Match 98.4%; Score 854; DB 3; Length 174;
Best Local Similarity 98.3%; Pred. No. 3.4e-91;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDTRYKKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDSF 120
DB 61 FAVDTRYKKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDSF 120

QY 121 SQTSLGLVLTGVSAYATPNDVLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174
DB 121 SQTSLGLVLTGVSAYATPNDVLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 3

US-08-913-362-30
; Sequence 30, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-913-362-30

Query Match 96.6%; Score 838.5; DB 3; Length 175;
Best Local Similarity 97.1%; Pred. No. 2.2e-89;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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DB 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDTRYKKNYK-ARSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 119
DB 61 FAVDTRYKKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 120

QY 120 PSOTSIGLVLTGVSAYATPNDVLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174
DB 120 PSOTSIGLVLTGVSAYATPNDVLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174

Db 121 FSQTSXGLGLAGVSAYATPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 175

RESULT 4

US-08-913-362-8
; Sequence 8, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-913-362-8

Query Match 95.0%; Score 825; DB 3; Length 174;
Best Local Similarity 94.3%; Pred. No. 7.9e-88;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALAALIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120

Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYFGARLSLNRAVAHLAGSDSF 120

QY 121 SQTSLGLVLTGVSAYATPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

Db 121 SKTSAGLGLAGVSAYATPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

RESULT 5

US-08-913-362-4
; Sequence 4, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-913-362-4

Query Match 95.0%; Score 824.5; DB 3; Length 175;
Best Local Similarity 95.4%; Pred. No. 9.1e-88;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALAALIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDS 119

Db 61 FAVDYTRYKNYKQVPESTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDS 120

QY 120 FSQTSIGLGLVLTGVSAYATPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

Db 121 FSQTSIGLGLAGVSAYATPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 175

RESULT 6.

US-08-127-499A-20
; Sequence 20, Application US/08127499A
; Patent No. 5510264

GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:

```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-482-847-20

Query Match 15.6%; Score 135; DB 1; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.3e-07;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATIALALPAALAEAGSGFYVQADAAH-----AKASSSLGS-----AKG 45
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 15 SSLLSSFAQAASEDRSPFYVQADLAVAAERITHDYPQATGANNTSTVSDYFRNIRAH 74

QY 46 FPRISAGRYINDLRPAVDYTRYKNY-----KAPSTDPK 79
   ||::||| ||::||| ||::||| ||::|||
Db 75 IHPRVSGVDFGWRIAADYASRYKWNNNKNYSVNTKELENKNNKKDLKTENQENGTFFHA 134

QY 80 LYSIGASAIYDPTDSPVKPYLGARLSLN--RASVD 113
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 135 ASLGLSALIYDFLKGKFPYIGARVAYGHVRHSID 170

RESULT 8
US-08-913-362-26
; Sequence 26, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josée
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768

```


REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO. 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
US-08-913-362-26

Query Match 15.3%; Score 133; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
Db 1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

RESULT 9

US-09-540-236-2245
Sequence 2245, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2245
LENGTH: 98
TYPE: PRT
ORGANISM: M. catarrhalis
US-09-540-236-2245

Query Match 13.1%; Score 113.5; DB 4; Length 98;
Best Local Similarity 37.9%; Pred. No. 1.8e-05;
Matches 22; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

QY 122 QTSIGLVLTGVSATVNVLDAGRYNYIG---KNTVKNVRSGE--LSGVVRVKF 174
Db 41 ETKVGFVLAGAQAYNQLSDAGVEYNLYGKYDKLDTASKAKAHOYGAQVGLRHF 98

RESULT 10

US-09-489-039A-13699
Sequence 13699, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13699
LENGTH: 187
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13699

Query Match 12.6%; Score 109.5; DB 4; Length 187;

Best Local Similarity 25.2%; Pred. No. 0.00014;
Matches 51; Conservative 26; Mismatches 78; Indels 47; Gaps 7;
QY 1 MKKALATLIA--LALPAALAEAGSGFYVQADAAHAKASSLSGSAK-----44
Db 5 MKSIAAKVAVTIALGASSAACAAVNLHGEAGFTNLSASFGAGEPGMTFSSQWAHSDN 64
QY 45 -GFSPRISAGYRINDLRPAVDYTRYKNYKAPSTDFKLYSIGASAIY----DFDTQSPVKP 99
Db 65 DGDVGLGMGYNFGP-----LMTLGGKAVYLNPKDDEGYATAA 106
QY 100 YLGARLSINRASVDLGGSDSFSQTSIGLV-----LTGVSVATPNVDLDAGVRY-NYI 152
Db 107 GGAELPLGQ-YFTLFGEGYSPDSMSSGVDEYVANNAGVRLNVRPSLNIEAGYRIIDMA 165
QY 153 GKVTNVKNVRSGLSVGVVRVKF 174
Db 166 GKDNDRNTLADGAYAGVNFVF 187

RESULT 11

US-09-543-681A-7922
Sequence 7922, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7922
LENGTH: 384
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7922

Query Match 12.0%; Score 104.5; DB 4; Length 384;
Best Local Similarity 26.1%; Pred. No. 0.0016;
Matches 55; Conservative 27; Mismatches 86; Indels 43; Gaps 13;

QY 1 MKKALATLIAALPAALAEAGSG-----FYVQADAAHAKASS-----SLGSARKF 46
Db 23 MKK---TAIALAVAAFAATAQAAPKDNWTYTGKLGWSQYQSTGNWWDGWNIGNGSTH 79
QY 47 SPRIS----AGYRIND---LRFVADYTRYKNYKAPSTD--FKLYSIGASAIYDFDTQSPV 97
Db 80 KDQICAGAFAGYQYNQVLFGLFELGYDLGRMAYKGSYNNNGAFKAQGIQLTTKLSYPVMDL 139
QY 98 KPY--LGARL-----SLNRASVDLGGSDSFSQTSIGLVL--TGVSVATPNVDLDAG 146
Db 140 DVTYTLGGWVRADSTATINATSA--GTQKRFSENDTGVSPVFGALGTAYAITPATRI 197
QY 147 YRY-NYIGKVTNVKNR--SGELSVGVVRVKF 174
Db 198 YQWNNIGDKGTL-NARPDNGMLSVGVAYRF 227

RESULT 12

US-09-543-681A-7684
Sequence 7684, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706

Search completed: May 19, 2005, 21:04:18
Job time : 113 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 20:34:09 ; Search time 69 Seconds
(without alignments)
242.634 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868
Sequence: 1 MKKALATLIALPAAALAE.....VNTVKNVRSBELSVGVKVF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	864	99.5	174	2 G81174	outer membrane pro
2	854	98.4	174	2 B81932	outer membrane pro
3	244.5	28.2	261	2 S16610	opacity protein op
4	242	27.9	260	2 S16611	opacity protein op
5	241.5	27.8	338	2 S16613	opacity protein op
6	241	27.8	258	2 S16612	opacity protein op
7	241	27.8	260	1 KONH0	opacity protein op
8	240.5	27.7	237	2 S36343	opacity protein op
9	240.5	27.7	257	2 S16614	opacity protein op
10	239	27.5	266	2 S16616	opacity protein op
11	238	27.4	258	2 S08514	opacity protein-re
12	237	27.3	254	2 S20043	opacity protein B
13	237	27.3	270	2 S04380	opacity protein P.
14	236.5	27.2	268	1 KONH2C	opacity protein P.
15	236	27.2	283	2 S72343	opacity protein op
16	232.5	26.8	234	2 S36329	opacity protein op
17	232.5	26.8	282	2 S16617	opacity protein op
18	232	26.7	234	2 S36342	opacity protein op
19	232	26.7	234	2 S36341	opacity protein op
20	231	26.6	233	2 S36350	opacity protein op
21	226	26.0	234	1 KONH8	opacity protein V2
22	226	26.0	234	2 S36348	opacity protein op
23	226	26.0	238	2 S36349	opacity protein op
24	226	26.0	261	2 S16619	opacity protein op
25	224.5	25.9	243	2 S36346	opacity protein op
26	221	25.5	248	2 PL0038	opacity protein D.
27	219	25.2	238	2 S36344	opacity protein op
28	217	25.0	178	2 F64124	opacity protein ho
29	215	24.8	239	2 S28630	opacity protein op

RESULT 1

G81174

Outer membrane protein Nega NMB0663 [imported] - Neisseria meningitidis (strain MC58 sero

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: G81174

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; PMID:20175755; PMID:10710307

A:Accession: G81174

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <TET>

A:Cross-references: UNIPROT:Q9RP17; GB:AE002420; GB:AE002098; NID:g7225876; PIDN:AAF41081

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0663

Query Match

Best Local Similarity 99.5%; Score 864; DB 2; Length 174;

Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFPKLYSIGASALYDEPTQSPVKPYLGARLSLNRSVDLGSDSF 120

Db 61 FAVDYTRYKNYKAPSTDFPKLYSIGASALYDEPTQSPVKPYLGARLSLNRSVDLGSDSF 120

QY 121 SQTSLGLGLVTCVSVYATPNVDLDAGYRNYIKGNTVKNVRSBELSVGVKVF 174

Db 121 SQTSLGLGLVTCVSVYATPNVDLDAGYRNYIKGNTVKNVRSBELSVGVKVF 174

RESULT 2

B81932

Outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain Z2491 serogro

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C:Accession: B81932

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagsals, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; PMID:20222556; PMID:10761919

A:Accession: B81932

A>Status: preliminary

A;Molecule type: DNA
A;Residues: 1-174 <PAR>
A;Cross-references: UNIPROT:P95372; GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB8414
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: nspA; NMA0862

Query Match 98.4%; Score 854; DB 2; Length 174;
Best Local Similarity 98.3%; Pred. No. 1.1e-68;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLALPAALAAAGCGFTVQADAAHAKASSLSGSAKGPSRISAGYRINDLR 60
Db 1 MKKALATLALPAALAAAGCGFTVQADAAHAKASSLSGSAKGPSRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDSF 120

QY 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGRVKF 174
Db 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGRVKF 174

RESULT 3
Sl6610
opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
N;Alternate names: outer membrane protein opak
C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
C;Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Accession: Sl6610
R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein
A;Reference number: Sl6610; MUID:92114767; PMID:1815562
A;Accession: Sl6610
A;Molecule type: DNA
A;Residues: 1-261 <BHA>
A;Cross-references: EMBL:X52364
A;Experimental source: strain MS11, variant 4.8
A;Note: the authors did not translate the sequence for the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
C;Genetics:
A;Gene: opak
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F;24-261/Product: opacity protein opak #status predicted <MAT>
F;34-42/Domain: transmembrane #status predicted <TM1>
F;43-75/Domain: extracellular #status predicted <EXT1>
F;51-61/Region: semivariable region
F;76-84/Domain: transmembrane #status predicted <TM2>
F;89-95/Domain: transmembrane #status predicted <TM3>
F;96-134/Domain: extracellular #status predicted <EXT2>
F;102-129/Region: hypervariable region HV1
F;135-149/Domain: transmembrane #status predicted <TM4>
F;166-212/Domain: transmembrane #status predicted <TM5>
F;171-218/Region: hypervariable region HV2
F;213-225/Domain: transmembrane #status predicted <TM6>
F;229-237/Domain: transmembrane #status predicted <TM7>
F;238-252/Domain: extracellular #status predicted <EXT4>
F;253-261/Domain: transmembrane #status predicted <TM8>

Query Match 28.2%; Score 244.5; DB 2; Length 261;
Best Local Similarity 29.9%; Pred. No. 2.3e-14;
Matches 73; Conservative 26; Mismatches 58; Indels 87; Gaps 10;

QY 15 AAALAEQ-ASGFTVQADAAHAKA-----SSLSGSAK-----FSPRI 50
Db 21 AQAASGNGCGFTVQADLAFAERITHTDPEPTGAKGTTISTVDFRNIRTHSHPRV 80

QY 51 SAGYRINDLRFAVDYTRYKNY-----KAPSTDFK-----LYS 82
Db 81 SVGYDFGGWRIRADYARYKWNKNYSVSIKELLRNKGNRTDLKAENQNGCTFFHAVSS 140

QY 83 IGASAIYDFDTQSPVKPYLGARLSLN--RASVD-----LGG-----116
Db 141 LGLSAVIDFKLNDKFKPYICARVAYGHVRHSIDSTKTKTTEVTILHGPCTTPTVYFGKNT 200

QY 117 -----SDSFSQTSIGLVLGTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGV 170
Db 201 QNAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGRYHYHWRLENTR-FKTHEASLGV 257

QY 171 RVKF 174
Db 258 RYRF 261

RESULT 4
Sl6611
opacity protein opaJ precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
N;Alternate names: outer membrane protein opa58
C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: Sl6611; S36345; S28624
R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein
A;Reference number: Sl6610; MUID:92114767; PMID:1815562
A;Accession: Sl6611
A;Molecule type: DNA
A;Residues: 1-260 <BHA>
A;Cross-references: UNIPROT:O04882; EMBL:X52371
A;Experimental source: strain MS11, variant 4.8
A;Note: the authors did not translate the sequence for the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F. EMBO J. 12, 641-650, 1993
A;Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms of Neisseria gonorrhoeae
A;Reference number: S36328; MUID:93178439; PMID:8440254
A;Accession: S36345
A;Molecule type: DNA
A;Residues: 24-260 <KUP>
A;Cross-references: EMBL:Z18937; NID:G49333; PIDN:CAA79370.1; PID:G940799
A;Experimental source: strain MS11, variant F3
A;Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
C;Genetics:
A;Gene: opaJ
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F;24-260/Product: opacity protein opaJ #status predicted <MAT>
F;34-42/Domain: transmembrane #status predicted <TM1>
F;43-74/Domain: extracellular #status predicted <EXT1>
F;51-60/Region: semivariable region
F;75-83/Domain: transmembrane #status predicted <TM2>
F;88-94/Domain: transmembrane #status predicted <TM3>
F;95-133/Domain: extracellular #status predicted <EXT2>
F;101-128/Region: hypervariable region HV1
F;134-148/Domain: transmembrane #status predicted <TM4>
F;154-164/Domain: transmembrane #status predicted <TM5>
F;165-211/Domain: extracellular #status predicted <EXT3>
F;170-217/Region: hypervariable region HV2
F;212-224/Domain: transmembrane #status predicted <TM6>
F;228-236/Domain: transmembrane #status predicted <TM7>
F;237-251/Domain: extracellular #status predicted <EXT4>
F;252-260/Domain: transmembrane #status predicted <TM8>

Query Match 27.9%; Score 242; DB 2; Length 260;
Best Local Similarity 29.5%; Pred. No. 3.9e-14;

```

Db      157 HPRVSVGVDFGGWRIADYARYRKWNKNKYSVDIKELNKNQKKDLKTENQNGTFHAV 216
               ||:||||| ||||| ||||| :||| |
Qy      81 YSIGASAIYDPTQSPVKPYLGARLSLN--RASVD-----LGG----- 116
               ||:||| ||||| ||||| ||||| ||||| |||||
Db      217 SSLGLSAVYDFKLNDKFKFYGARVAIGHVRHSIDTKTTFKLTSSYGGLNPVTVEEN 276
               ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      117 -----SDFSOTSIGLVLTGVSVAIVTNVDLDAGRYNYIKQVTVKRVSGELSGVGR 171
               ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      277 TQNAHQSNISRRVGLGVGIAGVGFDITPKLTDTSRYYHWGRLENTR-FKTHEASLGVR 335
               ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      172 VKF 174
               :|
Db      336 YRF 338
               :|

RESULT 6
SI6612
Opacity protein opaE precursor - Neisseria gonorrhoeae (strain MS11) (fragment)
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C>Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: SI6612
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.,
Mol. Microbiol. 5, 1989-1901, 1991
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded
A:Reference number: SI6610; MUID:92114767; PMID:1815562
A:Accession: SI6612
A:Molecule type: DNA
A:Residues: 1-258 <BHA>
A:Cross-references: EMBL:X52369
A:Experimental source: strain MS11, variant 4.8
A>Note: the authors did not translate the sequence for the signal peptide
A>Note: expression of opacity proteins is regulated by the number of translated
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opaE
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F:24-259/Product: opacity protein opaE #status predicted <MAT>
F:34-42/Domain: transmembrane #status predicted <TM1>
F:43-74/Domain: extracellular #status predicted <EXT1>
F:50-60/Region: semivariable region
F:75-83/Domain: transmembrane #status predicted <TM2>
F:88-94/Domain: transmembrane #status predicted <TM3>
F:95-131/Domain: extracellular #status predicted <EXT2>
F:101-125/Region: hypervariable region HV1
F:132-146/Domain: transmembrane #status predicted <TM4>
F:152-162/Domain: transmembrane #status predicted <TM5>
F:163-209/Domain: extracellular #status predicted <EXT3>
F:168-215/Region: hypervariable region HV2
F:210-222/Domain: transmembrane #status predicted <TM6>
F:226-234/Domain: transmembrane #status predicted <TM7>
F:235-249/Domain: extracellular #status predicted <EXT4>
F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match          27.8%; Score 241; DB 2; Length 258;
Best Local Similarity 29.7%; Pred No. 4,7e-14;
Matches       76; Conservative 26; Mismatches 68; Indels 86; Gaps 10

Qy      2 KKALATLATLALPAAALAE---ASGFYVQADAHA-----KASSSLGSAK----- 44
               ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      6 KKPSLLPSSLFLSSAAQAAGEDHGRGPVQADLAYAYEHITHDYPEPTGTCKDKISTVSD 65
               ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      45 -----GFSPRTSAGYRINDLRFAVDTRYK--NYKAPSTDFK----- 79
               ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      66 YFRNIRTHSIHPRVSVGVDFCGWRIAADYARYRKWNKNKYSVDIKELENNQNQRDLKTE 135
               ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      80 -----LYSIGASAIYDPTQSPVKPYLGARLSLN--RASVD-----LGG----- 116
               :||| ||||| ||||| ||||| ||||| ||||| |||||
Db      126 NOENGTFHAVSSLSGLSAVIDFKLNDKFPKYIGARVAYGHVRHSIDTKTTEVTTLIANGP 195
               :||| ||||| ||||| ||||| ||||| ||||| |||||

```

F;228-236/Domain:	transmembrane #status predicted <TM7>
F;237-251/Domain:	extracellular #status predicted <EXT4>
F;252-260/Domain:	transmembrane #status predicted <TM8>

Query Match	27.8%; Score 241; DB 1; Length 260;
Best Local Similarity	28.8%; Pred.No. 4.7e-14;
Matches	72; Conservative 30; Mismatches 64; Indels 84; Gaps 9;

QY	6	ATIIAIALPAALAEAGSGPYVQADAAHA-----KASSLSGSAKGSF-----	47
DB	14	SSLFFSAAQAASGEDGGRGYPVQADLAYAYEHITHDYPKPDPSPKGKISTVSDFRNIRT	73
QY	48	----PRISAGYRINDLARFAVDYTRY-----KNYKAPSTD--	77
DB	74	HSHIPRVGVGDGPGWRIRIADARYARKWSDNKYSIKMVRVKHNSNRKVLKTENOENG	133
QY	78	--FKLXIGSASAIYDFDTOSPVKPYILGARLSLN--RASVD-----LGG-	116
DB	134	SFHAVSSLGSLAIYDFQINDKFPIYGARVAVGHVRHSIDSTKKITGLLTFTTPGIMSGV	193
QY	117	-----SDSFQSOTSIGLVLTGVSAYATPNVDLDAGRYNYIGKVIVTKNVRSG	164
DB	194	YKVLRTPGAHRSDSI--VGLGVIAVGVDITPKLTLDAGRYHNWGRLNTR-FKTH	250
QY	165	ELSVGVGRVKF	174
DB	251	EASLGVRYRF	260

RESULT 8

S36343

opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)

N/Alternate names: outer membrane protein opa57

C/Species: Neisseria gonorrhoeae

A/Variety: strain MS11

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S36343; S28626

R/Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.

EMBO J. 12, 641-650, 1993

A/Title: Variable opacity (Opa) outer membrane proteins account for the cell tr

A/Reference number: S36328; PMID:93178439; PMID:8440254

A/Accession: S36343

A/Molecule type: DNA

A/Residues: 1-237 <KUP>

A/Cross-references: UNIPROT:Q04880; EMBL:Z18935; NID:g49331; PIDN:CNA79368.1; P

A/Experimental source: strain MS11, variant F3

A/Note: expression of opacity proteins is regulated by the number of translated o of repeats place the start codon in frame with the rest of the protein

C/Genetics:

A/Gene: opa57

C/Superfamily: opacity protein

C/Keywords: cell surface component; transmembrane protein

F;1-237/Product: opacity protein opa57 #status predicted <MAT>

F;11-19/Domain: transmembrane #status predicted <TM1>

F;20-51/Domain: extracellular #status predicted <EXT1>

F;28-37/Region: semivariable region

F;52-60/Domain: transmembrane #status predicted <TM2>

F;65-71/Domain: transmembrane #status predicted <TM3>

F;72-110/Domain: extracellular #status predicted <EXT2>

F;78-105/Region: hypervariable region HV1

F;111-125/Domain: transmembrane #status predicted <TM4>

F;131-141/Domain: transmembrane #status predicted <TM5>

F;142-188/Domain: extracellular #status predicted <EXT3>

F;147-194/Region: hypervariable region HV2

F;189-201/Domain: transmembrane #status predicted <TM6>

F;205-213/Domain: transmembrane #status predicted <TM7>

F;214-228/Domain: extracellular #status predicted <EXT4>

F;229-237/Domain: transmembrane #status predicted <TM8>

Query Match	27.7%; Score 240.5; DB 2; Length 237;
Best Local Similarity	29.6%; Pred.No. 4.7e-14;
Matches	71; Conservative 26; Mismatches 58; Indels 85; Gaps 9;

QY 17 ALAEGASGYVQADAHA-----KASSSLGS-----AKGSPRISAGY 54
 Db 1 ASDEGGPGYVQADLAYAYEHITHDYPEAPTAPNKKISTVSDYFRNIRTRSVHPRVSGY 60
 QY 55 RINDLRFADVTRYKNY-----KAPSTDFK-----LYSIGAS 86
 Db 61 DFGWRHIAADYARYRKNNKYSVSIKELLRNKNGNRTDLKAENQNGTTHAVSSLSLS 120
 QY 87 AIYDFDTPSPKPYLGARLSLN--RASVD-----LGG----- 116
 Db 121 AVYDFKLNKPKPYIGARVAYGHVHRHSIDSTKTKTEVTTLHGPGTTPTVVYKNTQDAH 180
 QY 117 --SDSFSQTSIGLVLTGVSAYATNVLDAGRYNYIGKNTVKNVSGELSGVGRVKF 174
 Db 181 RESDSIRR--VGLGAVAGVGIDITPNLTLDAGRYHYHWRLENTR-FKTHEASLGVRVRF 237

RESULT 9
 SI6614
 opacity protein opaF precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11
 C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: SI6614
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, I.
 Mol. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein
 A:Reference number: SI6610; PMID:92114767; PMID:1815562
 A:Accession: SI6614
 A:Molecule type: DNA
 A:Residues: 1-257 <BHA>
 A:Cross-references: EMBL:X52368
 A:Experimental source: strain MS11, variant 4.8
 A:Note: the authors did not translate the codon ACC for residue 206 as Ala and TAT for residue 207. The authors did not translate the sequence for the signal peptide
 A:Note: expression of opacity proteins is regulated by the number of translated repeat e of repeats place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opaF
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-257/Product: opacity protein opaF #status predicted <WAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-131/Domain: extracellular #status predicted <EXT2>
 F:101-126/Region: hypervariable region HV1
 F:132-146/Domain: transmembrane #status predicted <TM4>
 F:152-162/Domain: transmembrane #status predicted <TM5>
 F:163-208/Domain: extracellular #status predicted <EXT3>
 F:168-214/Region: hypervariable region HV2
 F:209-221/Domain: transmembrane #status predicted <TM6>
 F:225-233/Domain: transmembrane #status predicted <TM7>
 F:234-248/Domain: extracellular #status predicted <EXT4>
 F:249-257/Domain: transmembrane #status predicted <TM8>

Query Match 27.7%; Score 240.5; DB 2; Length 257;
 Best Local Similarity 29.2%; Pred. No. 5.2e-14;
 Matches 74; Conservative 26; Mismatches 72; Indels 81; Gaps 9;

QY 2 KKALATLIALAPAAALAE-----ASGFYVQADAHA-----KASSSLGS- 44
 Db 6 KKPSLLFSSLLFSSAAQAAGDHGPGVYVQADLAYAYEHITHDYPEPTGKDKLSTVD 65
 QY 45 -----GFSPRISAGRYNDRFAVDYTRYK--NYKAPSTDFK----- 79
 Db 66 YFRNIRTHSIHPRVSVGYDFGWRHIAADYARYRKWNKNKYSVDIKELKNQNKRDLDKTE 125
 QY 80 -----LYSIGASAIYDFDTPSPKPYLGARLSLN--RASVD-----LGG 116

Db 126 NOENGTTHAVSSLSLSAVYDFKLNKPKPYIGARVAYGHVHRHSIDSTKTKTKFLTSSVGG 185
 QY 117 -----SDSFSQTSIGLVLTGVSAYATNVLDAGRYNYIGKNTVKNV 161
 Db 186 LNPVTYVTEENTQNAHQHSNRRVGLGIAGVGPDIITPKLTLDTGRYHYHWRLENTR-F 244
 QY 162 RSGELSGVGRVKF 174
 Db 245 KTHEASLGVRVRF 257

RESULT 10
 SI6616
 opacity protein opaD precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11
 C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: SI6616
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, I.
 Mol. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein
 A:Reference number: SI6610; PMID:92114767; PMID:1815562
 A:Accession: SI6616
 A:Molecule type: DNA
 A:Residues: 1-266 <BHA>
 A:Cross-references: EMBL:X52372
 A:Experimental source: strain MS11, variant 4.8
 A:Note: the authors did not translate the sequence for the signal peptide
 A:Note: expression of opacity proteins is regulated by the number of translated repeat e of repeats place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opaD
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-266/Product: opacity protein opaD #status predicted <WAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-139/Domain: extracellular #status predicted <EXT2>
 F:101-134/Region: hypervariable region HV1
 F:140-154/Domain: transmembrane #status predicted <TM4>
 F:160-170/Domain: transmembrane #status predicted <TM5>
 F:171-217/Domain: extracellular #status predicted <EXT3>
 F:176-223/Region: hypervariable region HV2
 F:218-230/Domain: transmembrane #status predicted <TM6>
 F:234-242/Domain: transmembrane #status predicted <TM7>
 F:243-257/Domain: extracellular #status predicted <EXT4>
 F:258-266/Domain: transmembrane #status predicted <TM8>

Query Match 27.5%; Score 239; DB 2; Length 266;
 Best Local Similarity 29.0%; Pred. No. 7.3e-14;
 Matches 76; Conservative 26; Mismatches 70; Indels 90; Gaps 8;

QY 2 KKALATLIALAPAAALAE-----ASGFYVQADAHA-----KASSSLGS- 42
 Db 6 KKPSLLFSSLLFSSAAQAAGDHGPGVYVQADLAYAYEHITHDYPEPTAPKKAQLSTVD 65
 QY 43 -----AKGSPRISAGRYNDRFAVDYTRYK----- 69
 Db 66 YFRNIRTHSIHPRVSVGYDFGWRHIAADYARYRKWNKNKYSVNIKELLNNDNANSGSHL 125
 QY 70 NYKAPSTDFK-----LYSIGASAIYDFDTPSPKPYLGARLSL----- 107
 Db 126 NIKTRKTHRENGTTHAASSLSGLSAVDYDFDTPSPKPYIGMRVAYGHVHRHQRVSVQETI 185
 QY 108 -----NRASV-----DLGGSDFSQTSIGLVLTGVSAYATNVLDAGRYNYI 152
 Db 186 AVTYYPQNAASVTTNAPIRKLPHEHSRISLSLGFAGVAGVGDITPNLTLDAGRYHWNW 245
 QY 153 GKNTVKNVRSSELGSGVGRVKF 174

Fri May 20 10:37:41 2005

S72343
 opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063G)
 N:Alternate names: cell invasion protein opaH
 C:Species: Neisseria gonorrhoeae
 A:Variety: isolate 15063G
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S72343
 R:Waldbeser, L.S.; Ajioka, R.S.; Merz, A.J.; Puaoli, D.; Lin, L.; Thomas, M.; So, M.
 Mol. Microbiol. 13, 919-928, 1994
 A:title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell in
 A:Reference number: S72343; MUID:95115561; PMID:7815949
 A:Accession: S72343
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-283 <WAL>
 A:Cross-references: UNIPROT:Q50943; EMBL:U13708; NID:G535357; PIDN:AAA74082.1; PID:G5353
 A:Experimental source: isolate 15063G
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 A:Note: expression of opacity proteins is regulated by the number of translated repeat e
 of repeats place the start codon in frame with the rest of the protein
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-48/Domain: signal sequence #status predicted <SIG>
 F:49-283/Product: opacity protein opaH #status predicted <MAT>
 F:58-66/Domain: transmembrane #status predicted <TM1>
 F:67-98/Domain: extracellular #status predicted <EXT1>
 F:75-84/Region: semivariable region
 F:99-107/Domain: transmembrane #status predicted <TM2>
 F:112-118/Domain: transmembrane #status predicted <TM3>
 F:119-155/Domain: extracellular #status predicted <EXT2>
 F:125-150/Region: hypervariable region HV1
 F:156-170/Domain: transmembrane #status predicted <TM4>
 F:176-186/Domain: transmembrane #status predicted <TM5>
 F:187-234/Domain: extracellular #status predicted <EXT3>
 F:192-240/Region: hypervariable region HV2
 F:235-247/Domain: transmembrane #status predicted <TM6>
 F:251-259/Domain: transmembrane #status predicted <TM7>
 F:260-274/Domain: extracellular #status predicted <EXT4>
 F:275-283/Domain: transmembrane #status predicted <TM8>

Query Match 27.2%; Score 236; DB 2; Length 283;
 Best Local Similarity 27.9%; Pred. No. 1.5e-13;
 Matches 68; Conservative 29; Mismatches 67; Indels 80; Gaps 7;

QY	10	ALALPAALAEAGSGFYQADAAHAKA-----SSSLGSAGK-----FS 47
DB	41	SLLSAAQAASEAMRGYPYQADLAFAAERITHDYPEPTGKGTISTVSDYFNIRTHSVH 100
QY	48	PRISAGYRINDLRFADVTRYKNY-----KAPS-----TDPKLY 81
DB	101	PRVSVGYDFGGWRIAADYARYKWNKNYSVNIERVQEAHSNRIDLKAEQNGTFHVS 160
QY	82	STGASAIYDFDTQSPVKYLGARLSLN--RASVDL-----114
DB	161	SIGLSAVYDFKLNDRKFPYIGARVAYGVRHSIDSTKTKILTSTFYGVATKPTYDIGP 220
QY	115	-----CGSDSFSQTSIGLGLVLTGVSVAVTPNVLDLAGRYNYIGKNTVKNVRSGLSVGV 170
DB	221	KTQDAHQESNSIRRVGLGVGIAGVGFDITPKLTDIGYHYWGRLENTN-FKTHEASLGM 279
QY	171	RVKF 174
DB	280	RYRF 283

Search completed: May 19, 2005, 21:02:19
 Job time : 70 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 19, 2005, 20:24:55 ; Search time 357 Seconds
(without alignments)
249.585 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868

Sequence: 1 MKKALATLIALPAAALAE.....VNTVNVRSGLSVGVKVF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	2 P96943	P96943 neisseria m
2	864	99.5	174	2 Q7DDM2	Q7ddm2 neisseria m
3	864	99.5	174	2 Q9RP17	Q9rp17 neisseria m
4	857	98.7	174	2 Q9R2R1	Q9r2r1 neisseria m
5	854	98.4	174	2 P95372	P95372 neisseria m
6	854	98.4	174	2 Q7AR60	Q7ar60 neisseria m
7	852	98.2	174	2 Q9RP16	Q9rp16 neisseria m
8	846	97.5	174	2 Q9RP18	Q9rp18 neisseria m
9	825	95.0	174	2 P95343	P95343 neisseria g
10	824.5	95.0	175	2 P95371	P95371 neisseria m
11	303.5	35.0	177	2 Q6SRV6	Q6srv6 manheimia
12	256	23.5	226	2 Q85TE2	Q8ste2 manheimia
13	247	28.5	256	2 Q51124	Q51124 neisseria m
14	246.5	28.4	186	2 Q9CM19	Q9cm19 pasteurella
15	244	28.1	234	2 Q07280	Q07280 neisseria m
16	244	28.1	234	2 Q9R7I9	Q9r7i9 neisseria m
17	243	28.0	234	2 Q9R7I8	Q9r7i8 neisseria m
18	241.5	27.8	232	2 Q9K4T9	Q9k4t9 neisseria l
19	241.5	27.8	241	2 Q9AE80	Q9ae80 neisseria l
20	240.5	27.7	230	2 Q9R9A7	Q9r9a7 neisseria m
21	240.5	27.7	237	1 OPAP_NEIGO	Q04880 neisseria g
22	240	27.6	241	2 Q9K4T4	Q9k4t4 neisseria l
23	240	27.6	256	2 Q51126	Q51126 neisseria m
24	240	27.6	259	2 Q51125	Q51125 neisseria m
25	239.5	27.6	232	2 Q9R3P5	Q9r3p5 neisseria m
26	239	27.5	260	1 OPRI_NEIMC	P10170 neisseria m
27	238.5	27.5	257	2 Q50929	Q50929 neisseria f
28	238	27.4	234	2 Q07287	Q07287 neisseria m
29	238	27.4	237	2 Q31176	Q31176 neisseria m
30	237	27.3	239	2 Q7BW15	Q7bw15 neisseria m
31	237	27.3	262	2 Q33388	Q33388 neisseria m

RESULT 1

ID	P96943	PRELIMINARY;	PRT;	174 AA.
AC	P96943;			
DT	01-MAY-1997 (Tremblrel. 03, Created)			
DT	01-MAY-1997 (Tremblrel. 03, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Outer membrane protein precursor (Surface protein A).			
GN	Name=nsaA;			
OS	Neisseria meningitidis.			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=487;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=608B;			
RX	MEDLINE=97258610; PubMed=9104804;			
RA	Martin D., Cadieux N., Hamel J., Brodeur B.R.;			
RT	"Highly conserved Neisseria meningitidis surface protein confers protection against experimental infection.";			
RT	J. Exp. Med. 185:1173-1183(1997).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=608B;			
RC	MEDLINE=99270944; PubMed=10338491;			
RA	Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R.;			
RT	"Antigenic and molecular conservation of the gonococcal NspA protein.";			
RL	Infect. Immun. 67:2855-2861(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=608B;			
RX	MEDLINE=99386904; PubMed=10456958;			
RA	Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;			
RT	"Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein.";			
RL	Infect. Immun. 67:4955-4959(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=M986, NG6/88, and NGP165;			
RA	Moe G.R., Tan S., Granoff D.M.;			
RT	"Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";			
RL	Infect. Immun. 0:0-0(1999).			
DR	EMBL; U52066; AAC36000.1; -			
DR	EMBL; AF175680; AAD53283.1; -			
DR	EMBL; AF175682; AAD53285.1; -			
DR	HSSP; Q9RP17; 1P4T.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0015288; F:porin activity; IEA.			
DR	InterPro; IPR003394; Porin_opacity.			
DR	Pfam; PF02462; Opacity; I.			
KW	Signal.			

ALIGNMENTS

32	236.5	27.2	232	2	Q9K4T3	Q9k4t3 neisseria s
33	236.5	27.2	270	1	OMPC_NEIGO	P09888 neisseria g
34	236	27.2	270	2	Q9RQV4	Q9rqv4 neisseria m
35	236	27.2	283	2	Q50943	Q50943 neisseria g
36	235	27.1	236	1	OPAC_NEIGO	P11296 neisseria g
37	234.5	27.0	241	2	O07274	O07274 neisseria m
38	234	27.0	240	2	O07925	O07925 neisseria m
39	234	27.0	272	2	Q51013	Q51013 neisseria g
40	233.5	26.9	241	2	O07912	O07912 neisseria s
41	233.5	26.9	253	2	Q51303	Q51303 neisseria s
42	233	26.8	233	2	Q9K4T5	Q9k4t5 neisseria l
43	233	26.8	235	2	O30753	O30753 neisseria m
44	232.5	26.8	232	2	Q9R9A8	Q9r9a8 neisseria m
45	232.5	26.8	232	2	Q9R9A9	Q9r9a9 neisseria m

```

FT SIGNAL 1 19 Potential.
SQ SEQUENCE 174 AA; 18425 MW; E8B02767DDC6FE19 CRC64;

Query Match 100.0%; Score 868; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.5e-69;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSGISGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFKLYSGISGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120

QY 121 SQTSLGVLGTGSYAVTPNVDLDAGRYNYIGKNTVKNVRSGLSVGRVKF 174
DB 121 SQTSLGVLGTGSYAVTPNVDLDAGRYNYIGKNTVKNVRSGLSVGRVKF 174

RESULT 2
Q7DDM2 PRELIMINARY; PRT; 174 AA.
ID Q7DDM2
AC Q7DDM2; 2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Outer membrane protein NsgA.
GN OrderedLocusNames=NM0663;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Clifton H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qian H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815 (2000).
DR EMBL; AS002420; AAP41081.1; -.
DR TIGR; NMB0663; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Complete proteome.
SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 99.5%; Score 864; DB 2; Length 174;
Best Local Similarity 99.4%; Pred. No. 3.3e-69;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSGISGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFKLYSGISGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120

QY 121 SQTSLGVLGTGSYAVTPNVDLDAGRYNYIGKNTVKNVRSGLSVGRVKF 174
DB 121 SQTSLGVLGTGSYAVTPNVDLDAGRYNYIGKNTVKNVRSGLSVGRVKF 174

us-10-650-123-2.rup

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RESULT 3
Q9RP17 PRELIMINARY; PRT; 174 AA.
ID Q9RP17
AC Q9RP17;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Surface protein A.
GN Name=nsrA;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CU385;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0 (1999).
DR EMBL; AF175678; AAD53281.1; -.
DR PIR; G81174; G81174.
DR PDB; 1P4T; X-ray; A=20-174.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 99.5%; Score 864; DB 2; Length 174;
Best Local Similarity 99.4%; Pred. No. 3.3e-69;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSGISGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFKLYSGISGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120

QY 121 SQTSLGVLGTGSYAVTPNVDLDAGRYNYIGKNTVKNVRSGLSVGRVKF 174
DB 121 SQTSLGVLGTGSYAVTPNVDLDAGRYNYIGKNTVKNVRSGLSVGRVKF 174

RESULT 4
Q9R2R1 PRELIMINARY; PRT; 174 AA.
ID Q9R2R1
AC Q9R2R1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Surface protein A.
GN Name=nsrA;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M136, and BZ232;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0 (1999).
DR EMBL; AF175679; AAD53282.1; -.
DR EMBL; AF175677; AAD53280.1; -.
DR HSP; Q9RP17; 1P4T.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.

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DR InterPro: IPR003394; Porin_opacity.
 DR Pfam: PF02462; Opacity; 1.
 SQ SEQUENCE 174 AA; 18385 MW; ECF6F39A9286910E CRC64;

Query Match
 Best Local Similarity 98.7%; Score 857; DB 2; Length 174;
 Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARSLNRRASVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARSLNRRASVDLGGSDSF 120

QY 121 SQTSLGLGVLTCVSYAVTPNVLDAGYRNYIKGKNTVKNVRSGLSVGVVRVKF 174
 DB 121 SQTSLGLGVLTCVSYAVTPNVLDAGYRNYIKGKNTVKNVRSGLSVGVVRVKF 174

RESULT 5
 P95372
 ID P95372 PRELIMINARY; PRT; 174 AA.
 AC P95372;
 DT 01-MAY-1997 (TRENBLrel. 03, Created)
 DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Outer membrane protein precursor.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=24063;
 RX MEDLINE=99386904; PubMed=10456958;
 RA Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
 RT "Bactericidal and cross-protective activities of a monoclonal antibody
 RT directed against Neisseria meningitidis NspA outer membrane protein.";
 RL Infect. Immun. 67:4955-4959 (1999).
 DR EMBL: U52068; AAB41580.1; -.
 DR FIR; B81932; B81932.
 DR HSP; Q9RP17; 1P4T.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 DR InterPro: IPR003394; Porin_opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;

Query Match
 Best Local Similarity 98.4%; Score 854; DB 2; Length 174;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARSLNRRASVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARSLNRRASVDLGGSDSF 120

QY 121 SQTSLGLGVLTCVSYAVTPNVLDAGYRNYIKGKNTVKNVRSGLSVGVVRVKF 174
 DB 121 SQTSLGLGVLTCVSYAVTPNVLDAGYRNYIKGKNTVKNVRSGLSVGVVRVKF 174

RESULT 6
 Q7AR60
 ID Q7AR60 PRELIMINARY; PRT; 174 AA.
 AC Q7AR60;

DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Outer membrane protein.
 GN Name=nsrA; OrderedLocusNames=NMA0862;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
 RX MEDLINE=2222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman G., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli M., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis Z2491";
 RL Nature 404:502-506 (2000).
 DR EMBL; AL162754; CAB84143.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 DR InterPro: IPR003394; Porin_opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Complete proteome.
 SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;

Query Match
 Best Local Similarity 98.4%; Score 854; DB 2; Length 174;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARSLNRRASVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARSLNRRASVDLGGSDSF 120

QY 121 SQTSLGLGVLTCVSYAVTPNVLDAGYRNYIKGKNTVKNVRSGLSVGVVRVKF 174
 DB 121 SQTSLGLGVLTCVSYAVTPNVLDAGYRNYIKGKNTVKNVRSGLSVGVVRVKF 174

RESULT 7
 Q9RP16
 ID Q9RP16 PRELIMINARY; PRT; 174 AA.
 AC Q9RP16;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Surface protein A.
 GN Name=nsrA;
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NG3/88;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 RT among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0 (1999).
 DR EMBL; AF175681; AAD53284.1; -.
 DR HSP; Q9RP17; 1P4T.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 DR InterPro: IPR003394; Porin_opacity.
 DR Pfam; PF02462; Opacity; 1.


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Query Match      95.0%; Score 824.5; DB 2; Length 175;
Best Local Similarity 95.4%; Pred. No. 1.1e-65;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
   |||||
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
   |||||

QY 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDS 119
   |||||
DB 61 FAVDYTRYKNYKQVSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDS 120
   |||||

QY 120 FQSTSGIGLVLTGVSAYTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
   |||||
DB 121 FQSTSGIGLVLAGVSAYTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 175
   |||||

RESULT 11
Q5SRV6 PRELIMINARY; PRT; 177 AA.
AC Q65RV6;
DT 25-OCT-2004 (TremBLrel. 28, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=MS1697;
OS Mannheimia succiniciproducens MBEL55E.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP SEQUENCE FROM N.A.
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 0:0-0(2004).
DR EMBL; AE016827; AAU38304.1; -.
KW Hypothetical protein.
SQ SEQUENCE 177 AA; 18969 MW; B6ACF0AA75915B57 CRC64;

Query Match      35.0%; Score 303.5; DB 2; Length 177;
Best Local Similarity 40.2%; Pred. No. 3.8e-19;
Matches 74; Conservative 25; Mismatches 68; Indels 17; Gaps 6;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 59
   |||||
DB 1 MKKTLTALIALAMVSAQA-----NYYVEGNAGYSKIKSGEVSDHRFSPNALGYDTGDM 56
   |||||

QY 60 RFADVTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDL----- 114
   |||||
DB 57 RYADYTHYKSTDCNSEVKAHGFVSALYDIEVSPVKPYIGARLSAN--DIDAKEKR 114
   |||||

QY 115 -GGSDFSQT---STGLGLVLTGVSAYTPNVDLDAGYRNYIGKNTVKNVRSGLSVGV 170
   |||||
DB 115 SCSRIKETDSYKLYGALAGVQVQAKVDSLNGGVNRLGKANG-HNINQYAKVGV 173
   |||||

QY 171 RVKF 174
DB 174 RYDF 177

RESULT 12
Q5STE2 PRELIMINARY; PRT; 226 AA.
AC Q6STE2;
DT 25-OCT-2004 (TremBLrel. 28, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=MS1161;
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OS Mannheimia succiniciproducens MBEL55E.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP SEQUENCE FROM N.A.
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 0:0-0(2004).
DR EMBL; AE016827; AAU37768.1; -.
KW Hypothetical protein.
SQ SEQUENCE 226 AA; 25460 MW; 106C558F9B4C1504 CRC64;

Query Match      29.5%; Score 256; DB 2; Length 226;
Best Local Similarity 35.1%; Pred. No. 8.6e-15;
Matches 72; Conservative 26; Mismatches 67; Indels 40; Gaps 8;

QY 1 MKKALATLIALPAAALAEAGS-GFYVQADAAHAKASSLSGSAK-----FSPR 49
   |||||
DB 31 MKK---TTLAIVAIGILAISSASANWYVQGVGVGYSKIKAS-----GMDLDPKDNVFDQR 82
   |||||

QY 50 ISAGYRINDLRFAVDYTRYKNYK-----APSTDFKLYSIGASAIYDFTQSP 96
   |||||
DB 83 ISAGYDFGDIRLAVDYSHIGAKDHYTLFRGEQWETSGTSTVETNSFGISAIYDFNLNTS 142
   |||||

QY 97 VKPYLGARLSLNRAVS-----DLGSSDSFSQ--TSIGLVLTGVSAYTPNVDLDAGVY 149
   |||||
DB 143 LMPYGVRLSENSLKFEDHWRDNSASEYSSTKTKFYGALAGVQYHLTDLNLLNVGVEY 202
   |||||

QY 150 NYICKVNTVKNVRSGLSVGVVRKF 174
DB 203 NRLGKVEVK-IHOYSKAGLRVNF 226

RESULT 13
Q51124 PRELIMINARY; PRT; 256 AA.
AC Q51124
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)
DT 01-MAY-2004 (TremBLrel. 26, Last annotation update)
DE Opacity outer membrane protein (Fragment).
GN Name=opa;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=24197;
RX MEDLINE=98129089; PubMed=9467908;
RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
RA Heckels J.E., Cannon J.G., Achtman M.;
RT "Recombinational reassortment among opa genes from ET-37 complex
RT Neisseria meningitidis isolates of diverse geographical origins.";
RL Microbiology 144:157-166(1998).
DR EMBL; U37255; AAC46101.1; -.
DR FIR; B60119; B60119.
DR FIR; S77737; S77737.
DR HSSP; Q9RP17; 1P4T.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; I.
FT NON TER 1
SQ SEQUENCE 256 AA; 28335 MW; 9D41C6079C6DD13F CRC64;

Query Match      28.5%; Score 247; DB 2; Length 256;
Best Local Similarity 28.3%; Pred. No. 6.3e-14;
Matches 69; Conservative 33; Mismatches 64; Indels 78; Gaps 7;
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